GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 16, 2004, 15:53:20 ; Search time 41 Seconds
(without alignments)
882.675 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1238	100.0	228	21	AAB16955	Human IgG1 Fc prot
2	1238	100.0	228	21	AAY96529	Human IgG1 Fc chai
3	1238	100.0	228	22	AAB98953	Human IgG1 Fc regi
4	1238	100.0	228	23	AAU81074	Human IgG1 Fc. Ho
5	1238	100.0	228	23	ABB73410	Human immunoglobul
6	1238	100.0	228	23	AAE14310	Human immunoglobul
7	1238	100.0	228	23	AAU73018	Human immunoglobul
8	1238	100.0	228	23	AAG66012	Human immunoglobul
9	1238	100.0	228	23	ABB04279	Human IgG1 Fc doma
10	1238	100.0	228	24	ABJ38267	Human IgG1 Fc prot
11	1238	100.0	243	21	AAB17957	Fc-MMP inhibitor f
12	1238	100.0	243	23	ABB73425	Fc-MMP inhibitor f
13	1238	100.0	247	21	AAB16958	Fc-TMP protein seq
14	1238	100.0	247	23	ABB73411	Fc-TPO mimetic pep
15	1238	100.0	248	21	AAB17951	Fc-TNF-alpha inhib
16	1238	100.0	248	21	AAB17953	Fc-IL-1 antagonist
17	1238	100.0	248	23	ABB73419	Fc-TNF-alpha inhib
18	1238	100.0	248	23	ABB73421	Fc-interleukin 1 (
19	1238	100.0	252	21	AAB17955	Fc-VEGF antagonist
20	1238	100.0	252	23	ABB73423	Fc-VEGF antagonist
21	1238	100.0	253	21	AAB16964	Fc-EMP protein seq
22	1238	100.0	253	23	ABB73415	Fc-EPO mimetic pep
23	1238	100.0	268	21	AAB16959	Fc-TMP-TMP protein
24	1238	100.0	268	23	ABB73412	Fc-TMP-TMP amino a
25	1238	100.0	269	21	AAY96531	Human IgG1 Fc TMP
26	1238	100.0	277	21	AAB16967	Fc-EMP-EMP protein
27	1238	100.0	277	23	ABB73418	Fc-EMP-EMP nucleic
28	1238	100.0	282	23	AAU81169	Echistatin/IgG Fc
29	1238	100.0	374	19	AAW83963	Recombinant human
30	1238	100.0	374	19	AAW49075	Recombinant human
31	1238	100.0	401	22	AAY72922	Human met-Fc (lack
32	1238	100.0	401	22	AAB80904	Human metFcdeltaC-
33	1234	99.7	229	24	ABU07950	Human IgG Fc fragm
34	1234	99.7	235	20	AAY01372	Amino acid sequenc
35	1234	99.7	248	24	ABJ38332	TALL-1 inhibitory
36	1234	99.7	248	24	ABJ38333	TALL-1 inhibitory
37	1234	99.7	248	24	ABJ38334	TALL-1 inhibitory
38	1234	99.7	252	24	ABJ38335	TALL-1 inhibitory
39	1234	99.7	252	24	ABJ38336	TALL-1 inhibitory
40	1234	99.7	252	24	ABJ38337	TALL-1 inhibitory
41	1234	99.7	252	24	ABJ38338	TALL-1 inhibitory
42	1234	99.7	252	24	ABJ38339	TALL-1 inhibitory
43	1234	99.7	252	24	ABJ38340	TALL-1 inhibitory
44	1234	99.7	252	24	ABJ38341	TALL-1 inhibitory
45	1234	99.7	252	24	ABJ38342	TALL-1 inhibitory

ALIGNMENTS

RESULT 1
AAB16955
ID AAB16955 standard; Protein; 228 AA.
XX
AC AAB16955;
XX
DT 31-OCT-2000 (first entry)
XX
DE Human IgG1 Fc protein sequence SEQ ID NO:2.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX
OS Homo sapiens.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US25044.
XX
PR 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR N-PSDB; AAA69443.
XX
PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX
PS Claim 7; Page 176-177; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein

CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 21; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 2
AAY96529
ID AAY96529 standard; Protein; 228 AA.
XX
AC AAY96529;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human IgG1 Fc chain.
XX
KW Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
KW megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
KW anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
XX
OS Homo sapiens.
XX
PN WO200024770-A2.
XX
PD 04-MAY-2000.
XX
PF 22-OCT-1999; 99WO-US24834.
XX
PR 23-OCT-1998; 98US-0105348.
XX
PA (AMGE-) AMGEN INC.
XX
PI Liu C, Feige U, Cheetham J;
XX
DR WPI; 2000-365108/31.
DR N-PSDB; AAA29220.

XX
PT Thrombopoietic peptides which activate mpl receptors and increase the
PT production of platelets or platelet precursors, useful for treatment of
PT diseases which involve thombocytopenia
XX
PS Disclosure; Page 76-77; 91pp; English.
XX
CC A compound which binds to an mpl receptor comprising a thrombopoietin
CC mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2],
CC is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
CC 10 to 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2,
CC X_2-X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_3, and
CC X_1-X_1_4. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A;
CC X_4 = P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N,
CC or E; X_9 = W, Y or F; X_1_0 = L, I, V, A, F, M, or K; X_1_1 = A, I, V,
CC L, F, S, T, K, H, or E; X_1_2 = A, I, V, L, F, G, S, or Q; X_1_3 = R, K,
CC T, V, N, Q or G; X_1_4 = A, I, V, L, F, T, R, E, or G; L_1 = linker
CC comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and
CC activate the c-Mpl receptor which mediates the activity of endogenous
CC thrombopoietin. The TMPs are useful for increasing the production of
CC platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
CC is useful for treatment of diseases which involve thombocytopenia, e.g.
CC aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
CC virus associated ITP, and systemic lupus erythematosus.
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 21; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 3
AAB98953
ID AAB98953 standard; Protein; 228 AA.
XX
AC AAB98953;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human IgG1 Fc region.

XX
KW Human; IgG1; immunoglobulin; Fc region; Fc fusion protein;
KW misfolding; therapy; cancer; osteoarthritis; AIDS; obesity;
KW inflammation; transplant rejection.
XX
OS Homo sapiens.
XX
PN WO200134638-A1.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-US30798.
XX
PR 12-NOV-1999; 99US-0165188.
PR 09-NOV-2000; 2000US-0709704.
XX
PA (AMGE-) AMGEN INC.
XX
PI Treuheit MJ, O'Conner SR, Kosky AA;
XX
DR WPI; 2001-335908/35.
DR N-PSDB; AAH25762.
XX
PT Correcting disulfide bond misfolds in Fc-containing proteins,
PT particularly therapeutic Fc-containing fusion proteins or antibodies,
PT by treatment with copper halide -
XX
PS Claim 30; Fig 5; 59pp; English.
XX
CC The present invention describes a process for preparing a
CC pharmacologically active compound, involving preparing a compound
CC comprising an immunoglobulin Fc domain fused to a protein of interest,
CC treating the compound with a copper(II) halide and isolating the treated
CC molecule. This can be used to correct misfolding of Fc domain containing
CC proteins, for use in therapeutic agents which may be used in the
CC treatment of cancer, inflammation, transplant rejection, AIDS,
CC osteoarthritis and obesity. The present sequence is the IgG1 Fc domain.
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 22; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 4
AAU81074
ID   AAU81074 standard; Protein; 228 AA.
XX
AC   AAU81074;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human IgG1 Fc.
XX
KW   Human; IgG Fc; anticoagulant; thrombolytic; cytostatic;
KW   antiinflammatory; immunosuppressive; osteopathic; antagonist;
KW   laminin; saw-scaled viper; echistatin; integrin; selectin; vinculin;
KW   platelet aggregation; angiogenesis; tumour; inflammation;
KW   autoimmune disease; rheumatoid arthritis; osteoporosis.
XX
OS   Homo sapiens.
XX
PN   WO200181377-A2.
XX
PD   01-NOV-2001.
XX
PF   23-APR-2001; 2001WO-US13069.
XX
PR   21-APR-2000; 2000US-198919P.
PR   03-MAY-2000; 2000US-201394P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Kohno T,  Lacey DL,  Boone TC;
XX
DR   WPI; 2002-062025/08.
DR   N-PSDB; ABK24097.
XX
PT   Composition comprising integrin or adhesion antagonistic peptide and
PT   vehicle, useful for treating or preventing platelet aggregation, has a
PT   longer half-life than free peptide  -
XX
PS   Claim 9; Fig 3; 68pp; English.
XX
CC   The invention relates to a composition comprising an integrin/adhesion
CC   antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides
CC   are based on laminin or saw-scaled viper echistatin and target integrin,
CC   selectin or vinculin.Also included are compounds of formula (Ia) and
CC   their multimers (X^1)_a-F^1-(X^2)_b where;
CC   F^1  = Fc domain;
CC   X^1 and X^2  = -(L^1)_c-P^1, (L^1)_c-P^1-(L^2)_d-P^2,
CC   (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-P^3 or
CC   (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-P^3-(L^4)_f-P^4;
CC   P^1-P^4  = same or different (I);
CC   L^1-L^4  = same or different linkers;
CC   a-f  = 0 or 1, provided at least one of a and b = 1,
CC   a nucleic acid that encodes (Ia), an expression vector containing the
```

CC nucleic acid, host cells containing the vector, producing a
CC pharmaceutically active compound (B) by covalently linking at least one
CC Fc domain to at least one amino acid sequence of a selected randomized
CC (I) and any of six laminin-related peptides (Ib). The compositions are
CC used prophylactically and therapeutically in the same way as (I), e.g. to
CC inhibit platelet aggregation or angiogenesis (tumours), or to treat
CC inflammation and autoimmune diseases (e.g. rheumatoid arthritis) and many
CC different forms of osteoporosis, also for diagnosis. Attaching the
CC vehicle (especially Fc domain) to (I) increases the half-life (free (I)
CC are normally degraded very quickly in vivo). The present sequence
CC is human IgG1 Fc which is used as a vehicle for the antagonists of
CC the invention.
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 23; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 5
ABB73410
ID ABB73410 standard; Protein; 228 AA.
XX
AC ABB73410;
XX
DT 05-APR-2002 (first entry)
XX
DE Human immunoglobulin G1 Fc (IgG1 Fc) amino acid SEQ ID NO:2.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;

KW Fanconi's syndrome.
XX
OS Homo sapiens.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14310.
XX
PR 03-MAY-2000; 2000US-0563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
DR N-PSDB; ABL35760.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -
XX
PS Claim 7; Fig 4; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 23; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

```
Qy          61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy         121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy         181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 6
AAE14310
ID AAE14310 standard; Protein; 228 AA.
XX
AC AAE14310;
XX
DT 07-MAR-2002 (first entry)
XX
DE Human immunoglobulin G (IgG1) Fc.
XX
KW Human; calcitonin; CT; CT receptor; Fc domain; therapy; osteoporosis;
KW immunoglobulin G; IgG; osteopathic.
XX
OS Homo sapiens.
XX
PN WO200183526-A2.
XX
PD 08-NOV-2001.
XX
PF 03-MAY-2001; 2001WO-US14320.
XX
PR 03-MAY-2000; 2000US-201511P.
PR 02-MAY-2001; 2001US-0847712.
XX
PA (AMGE-) AMGEN INC.
XX
PI Liu C, Marshall WS, Reynolds A;
XX
DR WPI; 2002-034503/04.
DR N-PSDB; AAD23840.
XX
PT Compositions comprising Calcitonin receptor modulator domains, useful
PT for treating osteoporosis -
XX
PS Claim 8; Fig 3; 64pp; English.
XX
CC The invention relates to therapeutic agents that modulate the
CC activity of calcitonin (CT) receptor. Modulators of CT receptor
CC comprise a CT receptor modulating domain and a vehicle such as a
CC polymer or an Fc domain, where the vehicle is covalently attached
CC to the CT receptor modulating domain. The compositions comprising
CC CT receptor modulating domains are used to treat osteoporosis.
CC The present sequence is human immunoglobulin G (IgG1) Fc protein

CC used in the invention.
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 23; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 7
AAU73018
ID AAU73018 standard; Protein; 228 AA.
XX
AC AAU73018;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human immunoglobulin G (IgG) Fc region.
XX
KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.
XX
OS Homo sapiens.
XX
PN WO200181415-A2.
XX
PD 01-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US13528.
XX
PR 27-APR-2000; 2000US-200053P.
PR 28-JUN-2000; 2000US-214860P.
PR 06-FEB-2001; 2001US-266673P.
PR 26-APR-2001; 2001US-0843221.

XX
PA (AMGE-) AMGEN INC.
XX
PI Kostenuik P, Liu C, Lacey DL;
XX
DR WPI; 2002-066435/09.
DR N-PSDB; AAS97392.
XX
PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -
XX
PS Claim 6; Figure 3; 107pp; English.
XX
CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 23; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 8
AAG66012
ID AAG66012 standard; Protein; 228 AA.
XX
AC AAG66012;
XX
DT 27-FEB-2002 (first entry)
XX
DE Human immunoglobulin (Ig) G1 Fc region sequence.
XX
KW Apo-AI; amphipathic; pharmaceutical; peptide mimic; antilipemic;
KW anti-HIV; virucide; immunoglobulin; IgG1.
XX
OS Homo sapiens.
XX
PN WO200181376-A2.
XX
PD 01-NOV-2001.
XX
PF 23-APR-2001; 2001WO-US13068.
XX
PR 21-APR-2000; 2000US-198920P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Kohno T;
XX
DR WPI; 2002-049262/06.
DR N-PSDB; AAI67658.
XX
PT Recombinant or modified therapeutic agents having Apo-AI amphipathic
PT helix peptide activity useful in treatment of hypercholesterolemia and
PT viral infections such as herpes simplex virus, human immunodeficiency
PT virus -
XX
PS Claim 8; Fig 3A-B; 49pp; English.
XX
CC The invention provides a composition comprising a therapeutic agent that
CC has activity similar to Apo-AI amphipathic helix peptide, but with better
CC pharmaceutical characteristics attached to a vehicle through the
CC peptide's N-terminus or C-terminus having a specified formula. The
CC peptide mimic has greater half-life compared to conventional Apo-AI
CC amphipathic helix peptide. The compositions are useful for treating
CC hypercholesterolemia and viral infection such as HIV, HSV. The present
CC sequence represents the human immunoglobulin (Ig) G1 Fc region which acts
CC as a vehicle.
XX
SQ Sequence 228 AA;

  Query Match   100.0%; Score 1238; DB 23; Length 228;
  Best Local Similarity   100.0%; Pred. No. 1.2e-91;
  Matches 228; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

```
Qy          61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy         121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy         181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 9
ABB04279
ID ABB04279 standard; Protein; 228 AA.
XX
AC ABB04279;
XX
DT 13-FEB-2002 (first entry)
XX
DE Human IgG1 Fc domain.
XX
KW Glucagon antagonist; antidiabetic; anti-hormonal; Fc domain;
KW non-insulin dependent diabetes mellitus; human; immunoglobulin G; IgG.
XX
OS Homo sapiens.
XX
PN WO200183527-A2.
XX
PD 08-NOV-2001.
XX
PF 03-MAY-2001; 2001WO-US14321.
XX
PR 03-MAY-2000; 2000US-201436P.
PR 02-MAY-2001; 2001US-0847249.
XX
PA (AMGE-) AMGEN INC.
XX
PI Marshall WS, Stark KL;
XX
DR WPI; 2002-017738/02.
DR N-PSDB; ABA03672.
XX
PT Compositions comprising glucagon antagonist domains, useful for
PT treating diabetes mellitus -
XX
PS Claim 8; Fig 2; 54pp; English.
XX
CC The invention relates to compositions comprising a glucagon antagonist
CC domain and a vehicle, such as a polymer (e.g. PEG or dextran) or,
CC preferably, an Fc domain. The vehicle is covalently attached to the
CC glucagon antagonist domain. The compositions are administered to
CC treat non-insulin dependent diabetes mellitus. The present sequence
CC is the human IgG Fc domain, which may be used as the vehicle
CC in the compositions of the invention.
XX

SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 23; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 10
ABJ38267
ID ABJ38267 standard; Protein; 228 AA.
XX
AC ABJ38267;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human IgG1 Fc protein SEQ ID No 2.
XX
KW TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease;
KW systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;
KW inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis;
KW Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;
KW glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
KW multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
KW gene therapy; human IgG1Fc; human.
XX
OS Homo sapiens.
XX
PN WO200292620-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US15273.
XX
PR 11-MAY-2001; 2001US-290196P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Min H, Hsu H;
XX
DR WPI; 2003-156719/15.
DR N-PSDB; ABT33856.

XX
PT New TALL-1-binding polypeptide, useful for modulating the activity of
PT TALL-1 and in treating, preventing or diagnosing a B-cell-mediated
PT autoimmune diseases, cancers or lymphomas -
XX
PS Claim 36; Fig 3; 236pp; English.
XX
CC The invention relates to a novel TALL-1-binding polypeptide comprising a
CC defined sequence in the specification. The composition is useful in
CC modulating the activity of TALL-1, and in treating, preventing,
CC ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune
CC disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or
CC lymphoma. The composition may also be used in treating inflammations
CC (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease,
CC asthma, atherosclerosis, cachexia, cirrhosis, diabetes,
CC glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple
CC myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis
CC and vasculitis. Disorders may be treated with the novel composition using
CC gene therapy. This sequence represents a human IgG1Fc protein relating to
CC the TALL-1 sequence of the invention.
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 24; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 11
AAB17957
ID AAB17957 standard; Protein; 243 AA.
XX
AC AAB17957;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-MMP inhibitor fusion protein sequence SEQ ID NO:1068.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;

KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US25044.
XX
PR 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR N-PSDB; AAA69507.
XX
PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX
PS Example 7; Page 585-586; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1238; DB 21; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.3e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

```
Qy          61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy         121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy         181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 12
ABB73425
ID ABB73425 standard; Protein; 243 AA.
XX
AC ABB73425;
XX
DT 05-APR-2002 (first entry)
XX
DE Fc-MMP inhibitor fusion nucleic acid SEQ ID NO:1067.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14310.
XX
PR 03-MAY-2000; 2000US-0563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
DR N-PSDB; ABL35775.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,

PT diabetic retinopathy, obesity, sleep disorders and infertility -
XX
PS Example 7; Fig 25A-B; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1238; DB 23; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.3e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 13
AAB16958
ID AAB16958 standard; Protein; 247 AA.
XX
AC AAB16958;
XX
DT 31-OCT-2000 (first entry)

XX
DE Fc-TMP protein sequence SEQ ID NO:6.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US25044.
XX
PR 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR N-PSDB; AAA69444.
XX
PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX
PS Claim 21; Page 179-180; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1238; DB 21; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.3e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 14
ABB73411
ID ABB73411 standard; Protein; 247 AA.
XX
AC ABB73411;
XX
DT 05-APR-2002 (first entry)
XX
DE Fc-TPO mimetic peptide (Fc-TMP) amino acid SEQ ID NO:6.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14310.
XX
PR 03-MAY-2000; 2000US-0563286.
XX
PA (AMGE-) AMGEN INC.
XX

PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
DR N-PSDB; ABL35761.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -
XX
PS Claim 21; Fig 7; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1238; DB 23; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.3e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 15
AAB17951
ID AAB17951 standard; Protein; 248 AA.
XX
AC AAB17951;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-TNF-alpha inhibitor fusion protein sequence SEQ ID NO:1056.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US25044.
XX
PR 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR N-PSDB; AAA69501.
XX
PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX
PS Example 4; Page 568-569; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein

CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 1238; DB 21; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.3e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

Search completed: January 16, 2004, 15:57:06
Job time : 42 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 16, 2004, 15:56:15 ; Search time 22 Seconds
(without alignments)
438.494 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1234	99.7	229	4	US-09-122-144-2	Sequence 2, Appli
2	1234	99.7	347	1	US-07-940-861-43	Sequence 43, Appl
3	1234	99.7	347	1	US-08-459-512-43	Sequence 43, Appl
4	1234	99.7	347	2	US-08-459-657-43	Sequence 43, Appl
5	1234	99.7	347	2	US-08-460-132-43	Sequence 43, Appl
6	1234	99.7	347	3	US-08-466-465-8	Sequence 8, Appli
7	1234	99.7	347	5	PCT-US92-02050-43	Sequence 43, Appl
8	1234	99.7	446	4	US-09-157-452B-12	Sequence 12, Appl
9	1234	99.7	482	4	US-09-189-129-2	Sequence 2, Appli
10	1233	99.6	232	2	US-08-595-043A-50	Sequence 50, Appl
11	1233	99.6	235	3	US-09-131-247-6	Sequence 6, Appli

12	1233	99.6	331	3	US-09-178-869-2	Sequence 2, Appli
13	1233	99.6	331	4	US-09-761-413-2	Sequence 2, Appli
14	1233	99.6	360	4	US-09-180-100-11	Sequence 11, Appl
15	1233	99.6	371	1	US-08-236-311-7	Sequence 7, Appli
16	1233	99.6	371	3	US-08-457-918-7	Sequence 7, Appli
17	1233	99.6	376	4	US-09-180-100-22	Sequence 22, Appl
18	1233	99.6	387	1	US-08-470-299-4	Sequence 4, Appli
19	1233	99.6	388	3	US-09-131-247-16	Sequence 16, Appl
20	1233	99.6	389	3	US-09-131-247-14	Sequence 14, Appl
21	1233	99.6	396	2	US-08-784-512-3	Sequence 3, Appli
22	1233	99.6	396	3	US-09-176-228-3	Sequence 3, Appli
23	1233	99.6	424	4	US-09-333-593A-8	Sequence 8, Appli
24	1233	99.6	424	5	PCT-US95-03866-12	Sequence 12, Appl
25	1233	99.6	424	5	PCT-US95-03866-14	Sequence 14, Appl
26	1233	99.6	437	5	PCT-US96-10043-11	Sequence 11, Appl
27	1233	99.6	442	5	PCT-US96-10043-9	Sequence 9, Appli
28	1233	99.6	446	3	US-08-397-411-7	Sequence 7, Appli
29	1233	99.6	449	1	US-08-458-516-13	Sequence 13, Appl
30	1233	99.6	459	1	US-08-157-101A-7	Sequence 7, Appli
31	1233	99.6	475	4	US-09-740-002-27	Sequence 27, Appl
32	1233	99.6	476	2	US-08-378-939-10	Sequence 10, Appl
33	1233	99.6	476	3	US-08-487-550-4	Sequence 4, Appli
34	1233	99.6	476	3	US-08-487-550-12	Sequence 12, Appl
35	1233	99.6	476	4	US-09-526-098-4	Sequence 4, Appli
36	1233	99.6	476	4	US-09-526-098-12	Sequence 12, Appl
37	1233	99.6	478	3	US-08-487-550-8	Sequence 8, Appli
38	1233	99.6	478	4	US-09-526-098-8	Sequence 8, Appli
39	1233	99.6	488	3	US-08-776-511-2	Sequence 2, Appli
40	1233	99.6	592	4	US-09-313-942-8	Sequence 8, Appli
41	1233	99.6	680	3	US-08-227-496C-15	Sequence 15, Appl
42	1233	99.6	691	4	US-09-313-942-20	Sequence 20, Appl
43	1233	99.6	694	4	US-09-313-942-22	Sequence 22, Appl
44	1233	99.6	859	4	US-09-313-942-7	Sequence 7, Appli
45	1233	99.6	951	4	US-09-313-942-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-122-144-2
; Sequence 2, Application US/09122144A
; Patent No. 6485726
; GENERAL INFORMATION:
; APPLICANT: Blumberg, Richard S.
; APPLICANT: Simister, Neil E.
; APPLICANT: Lencer, Wayne I.
; TITLE OF INVENTION: RECEPTOR SPECIFIC TRANSEPITHELIAL TRANSPORT OF THERAPEUTICS
; FILE REFERENCE: S1383/7003
; CURRENT APPLICATION NUMBER: US/09/122,144A
; CURRENT FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: US 09/122,144
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 2
; LENGTH: 229

```
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-122-144-2

  Query Match             99.7%;  Score 1234;  DB 4;  Length 229;
  Best Local Similarity   99.6%;  Pred. No. 3.5e-117;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 61

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 121

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 229


RESULT 2
US-07-940-861-43
; Sequence 43, Application US/07940861
; Patent No. 5547853
;  GENERAL INFORMATION:
;    APPLICANT:  BIOGEN, INC.
;    APPLICANT:  WALLNER, Barbara P.
;    APPLICANT:  MILLER, Glenn T.
;    APPLICANT:  ROSA, Margaret D.
;    TITLE OF INVENTION:  CD2-BINDING DOMAIN OF LYMPHOCYTE
;    TITLE OF INVENTION:  FUNCTION ASSOCIATED ANTIGEN 3
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  875 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022-6250
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/940,861
;      FILING DATE:  21-OCT-1992
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/02050
;      FILING DATE:  12-MAR-1992
;    PRIOR APPLICATION DATA:
```

```
;       APPLICATION NUMBER:  US 07/667,971
;       FILING DATE:  12-MAR-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/770,967
;       FILING DATE:  07-OCT-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  HALEY, James F., Jr.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  B151CIP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)715-0600
;       TELEFAX:  (212)715-0673
;       TELEX:  14-8367
;   INFORMATION FOR SEQ ID NO:  43:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  347 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-07-940-861-43

  Query Match             99.7%;  Score 1234;  DB 1;  Length 347;
  Best Local Similarity   99.6%;  Pred. No. 6.3e-117;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 179

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 299

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347


RESULT 3
US-08-459-512-43
; Sequence 43, Application US/08459512
; Patent No. 5728677
;  GENERAL INFORMATION:
;    APPLICANT:  BIOGEN, INC.
;    APPLICANT:  WALLNER, Barbara P.
;    APPLICANT:  MILLER, Glenn T.
;    APPLICANT:  ROSA, Margaret D.
;    TITLE OF INVENTION:  CD2-BINDING DOMAIN OF LYMPHOCYTE
;    TITLE OF INVENTION:  FUNCTION ASSOCIATED ANTIGEN 3
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  875 Third Avenue
```

```
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10022-6250
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/459,512
;       FILING DATE:  02-JUN-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US92/02050
;       FILING DATE:  12-MAR-1992
;       APPLICATION NUMBER:  US 07/667,971
;       FILING DATE:  12-MAR-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/770,967
;       FILING DATE:  07-OCT-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  HALEY, James F., Jr.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  B151CIP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)715-0600
;       TELEFAX:  (212)715-0673
;       TELEX:  14-8367
;   INFORMATION FOR SEQ ID NO:  43:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  347 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-459-512-43

  Query Match             99.7%;  Score 1234;  DB 1;  Length 347;
  Best Local Similarity   99.6%;  Pred. No. 6.3e-117;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 179

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 299

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
```

RESULT 4
US-08-459-657-43
; Sequence 43, Application US/08459657
; Patent No. 5914111
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALLNER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,657
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 12-MAR-1992
; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B151CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)715-0600
; TELEFAX: (212)715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-657-43

Query Match 99.7%; Score 1234; DB 2; Length 347;
Best Local Similarity 99.6%; Pred. No. 6.3e-117;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 179

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 299

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
```

```
RESULT 5
US-08-460-132-43
; Sequence 43, Application US/08460132
; Patent No. 5928643
;  GENERAL INFORMATION:
;    APPLICANT:  BIOGEN, INC.
;    APPLICANT:  WALLNER, Barbara P.
;    APPLICANT:  MILLER, Glenn T.
;    APPLICANT:  ROSA, Margaret D.
;    TITLE OF INVENTION:  CD2-BINDING DOMAIN OF LYMPHOCYTE
;    TITLE OF INVENTION:  FUNCTION ASSOCIATED ANTIGEN 3
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  875 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022-6250
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,132
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/940,861
;      FILING DATE:  21-OCT-1992
;      APPLICATION NUMBER:  PCT/US92/02050
;      FILING DATE:  12-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/667,971
;      FILING DATE:  12-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/770,967
;      FILING DATE:  07-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  HALEY, James F., Jr.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  B151CIP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)715-0600
;       TELEFAX:  (212)715-0673
;       TELEX:  14-8367
;   INFORMATION FOR SEQ ID NO:  43:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  347 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-460-132-43

  Query Match             99.7%;  Score 1234;  DB 2;  Length 347;
  Best Local Similarity   99.6%;  Pred. No. 6.3e-117;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 179

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 299

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347


RESULT 6
US-08-466-465-8
; Sequence 8, Application US/08466465
; Patent No. 6162432
;  GENERAL INFORMATION:
;     APPLICANT:  Wallner, Barbara P.
;     APPLICANT:  Cooper, Kevin D.
;     TITLE OF INVENTION:  Method of Prophylaxis or Treatment of Antigen
;     TITLE OF INVENTION:  Presenting Cell Driven Skin Conditions Using
;     TITLE OF INVENTION:  Inhibitors of the CD2/LFA-3 Interaction
;     NUMBER OF SEQUENCES:  8
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  LAHIVE & COCKFIELD
;       STREET:  60 State Street, Suite 510
;       CITY:  Boston
;       STATE:  Massachusetts
;       COUNTRY:  USA
;       ZIP:  02109-1875
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
```

```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/466,465
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US92/08755
;       FILING DATE:  06-OCT-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/862,022
;       FILING DATE:  12-APR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/770,969
;       FILING DATE:  07-OCT-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Myers, Louis (PLM)
;       REGISTRATION NUMBER:  35,965
;       REFERENCE/DOCKET NUMBER:  BGP-111CP
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  347 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-466-465-8

  Query Match             99.7%;  Score 1234;  DB 3;  Length 347;
  Best Local Similarity   99.6%;  Pred. No. 6.3e-117;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 179

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 299

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347


RESULT 7
PCT-US92-02050-43
; Sequence 43, Application PC/TUS9202050
;  GENERAL INFORMATION:
;     APPLICANT:  BIOGEN, INC.
;     APPLICANT:  WALLNER, Barbara P.
;     APPLICANT:  MILLER, Glenn T.
```

```
;     APPLICANT:  ROSA, Margaret D.
;     TITLE OF INVENTION:  CD2-BINDING DOMAIN OF LYMPHOCYTE
;     TITLE OF INVENTION:  FUNCTION ASSOCIATED ANTIGEN 3
;     NUMBER OF SEQUENCES:  43
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fish & Neave
;       STREET:  875 Third Avenue
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10022-6250
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US92/02050
;       FILING DATE:  19920312
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/667,971
;       FILING DATE:  12-MAR-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/770,967
;       FILING DATE:  07-OCT-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  HALEY, James F., Jr.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  B151CIP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)715-0600
;       TELEFAX:  (212)715-0673
;       TELEX:  14-8367
;   INFORMATION FOR SEQ ID NO:  43:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  347 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US92-02050-43

  Query Match             99.7%;  Score 1234;  DB 5;  Length 347;
  Best Local Similarity   99.6%;  Pred. No. 6.3e-117;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 179

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 299
```

```
Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347


RESULT 8
US-09-157-452B-12
; Sequence 12, Application US/09157452B
; Patent No. 6482409
; GENERAL INFORMATION:
;  APPLICANT: Lobb, Roy R.
;  APPLICANT:  Burkly, Linda C.
;  TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
;  FILE REFERENCE: 10274-004003
;  CURRENT APPLICATION NUMBER: US/09/157,452B
;  CURRENT FILING DATE:  1998-09-21
;  PRIOR APPLICATION NUMBER: US 08/950,660
;  PRIOR FILING DATE: 1997-10-15
;  PRIOR APPLICATION NUMBER: US 08/373,857
;  PRIOR FILING DATE: 1995-01-18
;  PRIOR APPLICATION NUMBER: US 08/284,603
;  PRIOR FILING DATE: 1994-08-11
;  PRIOR APPLICATION NUMBER: PCT/US93/00924
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: US 07/835,139
;  PRIOR FILING DATE: 1992-02-12
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 446
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-157-452B-12

  Query Match             99.7%;  Score 1234;  DB 4;  Length 446;
  Best Local Similarity   99.6%;  Pred. No. 9.1e-117;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 278

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 338

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 398

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 446


RESULT 9
```

```
US-09-189-129-2
; Sequence 2, Application US/09189129
; Patent No. 6323027
;  GENERAL INFORMATION:
;    APPLICANT:  Burkly, Linda C
;    APPLICANT:  Benjamin, Christopher D
;    APPLICANT:  Hession, Catherine A
;    APPLICANT:  Whitty, Adrian
;    TITLE OF INVENTION:  COMMON GAMMA CHAIN BLOCKING AGENTS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Biogen, Inc.
;      STREET:  14 Cambridge Center
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02142
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/189,129
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  A006 PCT CIP
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  60/017,466
;      FILING DATE:  10-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kaplan, Warren A.
;      REGISTRATION NUMBER:  34,199
;      REFERENCE/DOCKET NUMBER:  A006 PCT CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617 679-2000
;      TELEFAX:  617 679-2838
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  482 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
US-09-189-129-2

  Query Match             99.7%;  Score 1234;  DB 4;  Length 482;
  Best Local Similarity   99.6%;  Pred. No. 1e-116;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 314

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 374

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 434

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 482


RESULT 10
US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
;  GENERAL INFORMATION:
;    APPLICANT:  SGARLATO, GREGORY D.
;    TITLE OF INVENTION:  PROTEIN EXPRESSION SYSTEM
;    NUMBER OF SEQUENCES:  90
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MEDLEN & CARROLL
;      STREET:  220 MONTGOMERY STREET, SUITE 2200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/595,043A
;      FILING DATE:  31-JAN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  SGAR-00371
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 232 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-595-043A-50

  Query Match             99.6%;  Score 1233;  DB 2;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-117;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          6 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 125

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 185

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        186 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232


RESULT 11
US-09-131-247-6
; Sequence 6, Application US/09131247
; Patent No. 6294170
; GENERAL INFORMATION:
;  APPLICANT: Boone, Thomas C.
;  APPLICANT: Hershenson, Susan
;  APPLICANT: Bevilacqua, Michael P.
;  APPLICANT: Collins, David S.
;  TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
;  TITLE OF INVENTION: DISEASES
;  FILE REFERENCE: A-365F
;  CURRENT APPLICATION NUMBER: US/09/131,247
;  CURRENT FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 60/055,185
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: PCT/US 97/02131
;  EARLIER FILING DATE: 1997-02-10
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Human
US-09-131-247-6

  Query Match             99.6%;  Score 1233;  DB 3;  Length 235;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-117;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 68

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 128

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 188
```

```
Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 235


RESULT 12
US-09-178-869-2
; Sequence 2, Application US/09178869B
; Patent No. 6197294
; GENERAL INFORMATION:
;  APPLICANT: Tao, Weng
;  APPLICANT: Wong, Shou
;  APPLICANT: Hickey, William F
;  APPLICANT: Hammang, Joseph P.
;  APPLICANT: Baetge, E. Edward
;  TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
;  FILE REFERENCE: 17810-043
;  CURRENT APPLICATION NUMBER: US/09/178,869B
;  CURRENT FILING DATE: 1998-10-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 331
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-178-869-2

  Query Match             99.6%;  Score 1233;  DB 3;  Length 331;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-117;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 164

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 224

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 284

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 331


RESULT 13
US-09-761-413-2
; Sequence 2, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
;  APPLICANT: Tao, Weng
;  APPLICANT:  Wong, Shou
;  APPLICANT:  Hickey, William F
;  APPLICANT:  Hammang, Joseph P.
```

```
;  APPLICANT:  Baetge, E. Edward
;  TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
;  FILE REFERENCE: 17810-043
;  CURRENT APPLICATION NUMBER: US/09/761,413
;  CURRENT FILING DATE:  2001-01-16
;  PRIOR APPLICATION NUMBER: US/09/178,869
;  PRIOR FILING DATE: 1998-10-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 331
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-761-413-2

  Query Match             99.6%;  Score 1233;  DB 4;  Length 331;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-117;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 164

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 224

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 284

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        285 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 331


RESULT 14
US-09-180-100-11
; Sequence 11, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA, No. 6306395io
;  APPLICANT: NAGATA, Shigekazu
;  TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
;  FILE REFERENCE: 1110-207P
;  CURRENT APPLICATION NUMBER: US/09/180,100
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: PCT/JP97/01502
;  EARLIER FILING DATE: 1997-05-01
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-180-100-11
```

```
  Query Match             99.6%;  Score 1233;  DB 4;  Length 360;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-117;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 193

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 253

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 313

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        314 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 360


RESULT 15
US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5565335
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/236,311
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
```

```
;       FILING DATE:  02-OCT-1987
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Hasak, Janet E.
;       REGISTRATION NUMBER:  28,616
;       REFERENCE/DOCKET NUMBER:  444P1C2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-1896
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  371 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-236-311-7

  Query Match             99.6%;  Score 1233;  DB 1;  Length 371;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-117;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 204

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 264

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 324

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        325 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371


Search completed: January 16, 2004, 15:59:34
Job time : 23 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 16, 2004, 15:58:31 ; Search time 33 Seconds
(without alignments)
1412.779 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 762491 seqs, 204481190 residues

Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	1238	100.0	228	9	US-09-847-712-2	Sequence 2, Appli
2	1238	100.0	228	10	US-09-840-277-2	Sequence 2, Appli
3	1238	100.0	228	11	US-09-847-249A-2	Sequence 2, Appli
4	1238	100.0	228	11	US-09-843-221A-2	Sequence 2, Appli
5	1238	100.0	228	11	US-09-840-669B-2	Sequence 2, Appli
6	1238	100.0	228	12	US-10-269-806-32	Sequence 32, Appl
7	1238	100.0	228	12	US-10-145-206-2	Sequence 2, Appli
8	1238	100.0	243	12	US-10-269-806-152	Sequence 152, App
9	1238	100.0	250	12	US-10-269-695-243	Sequence 243, App
10	1238	100.0	250	12	US-10-410-998-243	Sequence 243, App
11	1238	100.0	282	10	US-09-840-277-109	Sequence 109, App
12	1238	100.0	401	12	US-09-389-782-8	Sequence 8, Appli
13	1234	99.7	229	14	US-10-215-297-2	Sequence 2, Appli
14	1234	99.7	229	15	US-10-215-298-2	Sequence 2, Appli
15	1234	99.7	248	12	US-10-145-206-111	Sequence 111, App
16	1234	99.7	248	12	US-10-145-206-112	Sequence 112, App
17	1234	99.7	248	12	US-10-145-206-113	Sequence 113, App
18	1234	99.7	252	12	US-10-145-206-114	Sequence 114, App
19	1234	99.7	252	12	US-10-145-206-115	Sequence 115, App
20	1234	99.7	252	12	US-10-145-206-116	Sequence 116, App
21	1234	99.7	252	12	US-10-145-206-117	Sequence 117, App
22	1234	99.7	252	12	US-10-145-206-118	Sequence 118, App
23	1234	99.7	252	12	US-10-145-206-119	Sequence 119, App
24	1234	99.7	252	12	US-10-145-206-120	Sequence 120, App
25	1234	99.7	252	12	US-10-145-206-121	Sequence 121, App
26	1234	99.7	252	12	US-10-145-206-122	Sequence 122, App
27	1234	99.7	261	12	US-10-435-608-6	Sequence 6, Appli
28	1234	99.7	266	12	US-10-390-566-8	Sequence 8, Appli
29	1234	99.7	266	12	US-10-390-566-15	Sequence 15, Appl
30	1234	99.7	266	12	US-10-390-566-21	Sequence 21, Appl
31	1234	99.7	266	12	US-10-390-566-28	Sequence 28, Appl
32	1234	99.7	293	12	US-10-145-206-123	Sequence 123, App
33	1234	99.7	293	12	US-10-145-206-124	Sequence 124, App
34	1234	99.7	302	15	US-10-115-192-12	Sequence 12, Appl
35	1234	99.7	347	9	US-09-796-033-8	Sequence 8, Appli
36	1234	99.7	347	9	US-09-730-465-8	Sequence 8, Appli
37	1234	99.7	347	12	US-10-329-599-8	Sequence 8, Appli
38	1234	99.7	347	14	US-10-091-236-17	Sequence 17, Appl
39	1234	99.7	347	15	US-10-091-313-7	Sequence 7, Appli
40	1234	99.7	347	15	US-10-091-268-7	Sequence 7, Appli
41	1234	99.7	360	12	US-10-390-566-7	Sequence 7, Appli
42	1234	99.7	360	12	US-10-390-566-14	Sequence 14, Appl
43	1234	99.7	360	12	US-10-390-566-20	Sequence 20, Appl
44	1234	99.7	360	12	US-10-390-566-27	Sequence 27, Appl
45	1234	99.7	367	12	US-10-390-566-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-847-712-2
; Sequence 2, Application US/09847712
; Patent No. US20020090646A1
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA

```
;  APPLICANT:  MARSHALL, WILLIAM S.
;  APPLICANT:  REYNOLDS, ANGELA
;  TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
;  FILE REFERENCE: A-684
;  CURRENT APPLICATION NUMBER: US/09/847,712
;  CURRENT FILING DATE:  2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,511
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-847-712-2

  Query Match             100.0%;  Score 1238;  DB 9;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-99;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 2
US-09-840-277-2
; Sequence 2, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  KOHNO, TADAHIKO
;  APPLICANT:  LACEY, DAVID LEE
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
;  FILE REFERENCE: A-688A
;  CURRENT APPLICATION NUMBER: US/09/840,277
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: 60/198,919
;  PRIOR FILING DATE: 2000-04-21
;  PRIOR APPLICATION NUMBER: 60/201,394
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
```

```
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-840-277-2

  Query Match             100.0%;  Score 1238;  DB 10;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-99;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 3
US-09-847-249A-2
; Sequence 2, Application US/09847249A
; Publication No. US20030032588A1
; GENERAL INFORMATION:
;  APPLICANT: MARSHALL, WILLIAM S.
;  APPLICANT:  STARK, KEVIN LEE
;  TITLE OF INVENTION: GLUCAGON ANTAGONIST
;  FILE REFERENCE: A-693
;  CURRENT APPLICATION NUMBER: US/09/847,249A
;  CURRENT FILING DATE:  2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,436
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-847-249A-2

  Query Match             100.0%;  Score 1238;  DB 11;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-99;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 4
US-09-843-221A-2
; Sequence 2, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-2

  Query Match           100.0%;  Score 1238;  DB 11;  Length 228;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-99;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 5
US-09-840-669B-2
; Sequence 2, Application US/09840669B
; Publication No. US20030040470A1
; GENERAL INFORMATION:
;  APPLICANT: KOHNO, TADAHIKO
;  TITLE OF INVENTION: APO-AI/AII PEPTIDE DERIVATIVES
;  FILE REFERENCE: A-690
;  CURRENT APPLICATION NUMBER: US/09/840,669B
;  CURRENT FILING DATE:  2002-06-07
;  PRIOR APPLICATION NUMBER: 60/198,920
;  PRIOR FILING DATE: 2000-04-21
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-840-669B-2

  Query Match           100.0%;  Score 1238;  DB 11;  Length 228;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-99;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 6
US-10-269-806-32
; Sequence 32, Application US/10269806
; Publication No. US20030176352A1
; GENERAL INFORMATION:
;  APPLICANT: Min, Hosung
;  APPLICANT:  Sitney, Karen
;  APPLICANT:  Hartley, Cynthia
;  TITLE OF INVENTION: Peptides and Related Compounds Having Thrombopoietic
Activity
;  FILE REFERENCE: A-750
;  CURRENT APPLICATION NUMBER: US/10/269,806
;  CURRENT FILING DATE:  2002-10-10
```

```
;  NUMBER OF SEQ ID NOS: 199
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthesized Peptide Sequence
US-10-269-806-32
```

Query Match 100.0%; Score 1238; DB 12; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.9e-99;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

```
RESULT 7
US-10-145-206-2
; Sequence 2, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
;  APPLICANT: MIN, HOSUNG
;  APPLICANT:  HSU, HAILING
;  APPLICANT:  ZIONG, FEI
;  TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
;  FILE REFERENCE: A-743
;  CURRENT APPLICATION NUMBER: US/10/145,206
;  CURRENT FILING DATE:  2002-05-13
;  PRIOR APPLICATION NUMBER: US 60/290,196
;  PRIOR FILING DATE: 2001-05-11
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-145-206-2
```

Query Match 100.0%; Score 1238; DB 12; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.9e-99;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 8
US-10-269-806-152
; Sequence 152, Application US/10269806
; Publication No. US20030176352A1
; GENERAL INFORMATION:
;  APPLICANT: Min, Hosung
;  APPLICANT:  Sitney, Karen
;  APPLICANT:  Hartley, Cynthia
;  TITLE OF INVENTION: Peptides and Related Compounds Having Thrombopoietic
Activity
;  FILE REFERENCE: A-750
;  CURRENT APPLICATION NUMBER: US/10/269,806
;  CURRENT FILING DATE:  2002-10-10
;  NUMBER OF SEQ ID NOS: 199
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 152
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthesized Peptide Sequence
US-10-269-806-152

  Query Match             100.0%;  Score 1238;  DB 12;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 2e-99;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 9
US-10-269-695-243
; Sequence 243, Application US/10269695
; Publication No. US20030229023A1
; GENERAL INFORMATION:
;  APPLICANT: OLINER, JONATHAN DANIEL
;  APPLICANT:  MIN, HOSUNG
;  TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
;  FILE REFERENCE: A-801A
;  CURRENT APPLICATION NUMBER: US/10/269,695
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/414,155
;  PRIOR FILING DATE: 2002-09-27
;  PRIOR APPLICATION NUMBER: US 60/328,624
;  PRIOR FILING DATE: 2001-10-11
;  NUMBER OF SEQ ID NOS: 359
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 243
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding peptide capable of binding to Ang-2
US-10-269-695-243

  Query Match           100.0%;  Score 1238;  DB 12;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-99;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 10
US-10-410-998-243
; Sequence 243, Application US/10410998
; Publication No. US20030236193A1
; GENERAL INFORMATION:
;  APPLICANT: OLINER, JONATHAN DANIEL
;  APPLICANT:  MIN, HOSUNG
```

```
;  TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
;  FILE REFERENCE: A-801A
;  CURRENT APPLICATION NUMBER: US/10/410,998
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US/10/269,695
;  PRIOR FILING DATE: 2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/414,155
;  PRIOR FILING DATE: 2002-09-27
;  PRIOR APPLICATION NUMBER: US 60/328,624
;  PRIOR FILING DATE: 2001-10-11
;  NUMBER OF SEQ ID NOS: 359
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 243
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding peptide capable of binding to Ang-2
US-10-410-998-243

  Query Match           100.0%;  Score 1238;  DB 12;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-99;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 11
US-09-840-277-109
; Sequence 109, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  KOHNO, TADAHIKO
;  APPLICANT:  LACEY, DAVID LEE
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
;  FILE REFERENCE: A-688A
;  CURRENT APPLICATION NUMBER: US/09/840,277
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: 60/198,919
;  PRIOR FILING DATE: 2000-04-21
;  PRIOR APPLICATION NUMBER: 60/201,394
```

```
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
;   LENGTH: 282
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Echistatin Fc-peptide
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: NdeI site
;   NAME/KEY: misc_feature
;   LOCATION: (854)..(854)
;   OTHER INFORMATION: BamHI site
US-09-840-277-109

  Query Match           100.0%;  Score 1238;  DB 10;  Length 282;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-99;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 12
US-09-389-782-8
; Sequence 8, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
;  APPLICANT: Wooden, Scott K.
;  APPLICANT: Mann, Michael B.
;  APPLICANT: Dunstan, Colin R.
;  TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
;  FILE REFERENCE: A-604
;  CURRENT APPLICATION NUMBER: US/09/389,782
;  CURRENT FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 401
;   TYPE: PRT
;   ORGANISM: Human
US-09-389-782-8
```

```
  Query Match             100.0%;  Score 1238;  DB 12;  Length 401;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-99;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 13
US-10-215-297-2
; Sequence 2, Application US/10215297
; Publication No. US20020192222A1
; GENERAL INFORMATION:
;  APPLICANT: Blumberg, Richard S.
;  APPLICANT:  Simister, Neil E.
;  APPLICANT:  Lencer, Wayne I.
;  TITLE OF INVENTION: RECEPTOR SPECIFIC TRANSEPITHELIAL TRANSPORT OF
;  TITLE OF INVENTION:  THERAPEUTICS
;  FILE REFERENCE: S1383/7003
;  CURRENT APPLICATION NUMBER: US/10/215,297
;  CURRENT FILING DATE:  2002-08-08
;  PRIOR APPLICATION NUMBER: US 08/578,171
;  PRIOR FILING DATE: 1995-12-29
;  PRIOR APPLICATION NUMBER: US 08/374,159
;  PRIOR FILING DATE: 1995-01-17
;  PRIOR APPLICATION NUMBER: US 09/122,144
;  PRIOR FILING DATE: 1998-07-24
;  NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 2
;   LENGTH: 229
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-215-297-2

  Query Match             99.7%;  Score 1234;  DB 14;  Length 229;
  Best Local Similarity   99.6%;  Pred. No. 4.2e-99;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 61

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 121

Qy         121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181

Qy         181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 229


RESULT 14
US-10-215-298-2
; Sequence 2, Application US/10215298
; Publication No. US20030012789A1
; GENERAL INFORMATION:
;  APPLICANT: Blumberg, Richard S.
;  APPLICANT:  Simister, Neil E.
;  APPLICANT:  Lencer, Wayne I.
;  TITLE OF INVENTION: RECEPTOR SPECIFIC TRANSEPITHELIAL TRANSPORT OF
THERAPEUTICS
;  FILE REFERENCE: S1383/7003
;  CURRENT APPLICATION NUMBER: US/10/215,298
;  CURRENT FILING DATE:  2002-08-08
;  PRIOR APPLICATION NUMBER: US 09/122,144
;  PRIOR FILING DATE: 1998-07-24
;  NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 2
;   LENGTH: 229
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-215-298-2

  Query Match             99.7%;  Score 1234;  DB 15;  Length 229;
  Best Local Similarity   99.6%;  Pred. No. 4.2e-99;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
                :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 61

Qy          61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 121

Qy         121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181

Qy         181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 229


RESULT 15
US-10-145-206-111
```

; Sequence 111, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 111
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TALL-1 inhibitory peptibodies
US-10-145-206-111

Query Match 99.7%; Score 1234; DB 12; Length 248;
Best Local Similarity 99.6%; Pred. No. 4.6e-99;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 80

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 140

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 200

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 248
```

Search completed: January 16, 2004, 16:04:07
Job time : 34 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 16, 2004, 15:55:25 ; Search time 20 Seconds
(without alignments)
1096.323 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1233	99.6	255	4	S31866	Ig gamma-1 chain C
2	1233	99.6	330	1	GHHU	Ig gamma-1 chain C
3	1227	99.1	374	2	S69339	Ig heavy chain V r
4	1180	95.3	234	2	PT0207	Ig gamma chain C r
5	1146	92.6	377	2	A23511	Ig gamma-3 chain C
6	1144	92.4	377	2	A60764	Ig gamma-3 chain C
7	1142.5	92.3	326	1	G2HU	Ig gamma-2 chain C
8	1135	91.7	327	1	G4HU	Ig gamma-4 chain C
9	1121	90.5	289	1	G3HUWI	Ig gamma-3 heavy c
10	918.5	74.2	323	1	GHRB	Ig gamma chain C r
11	906.5	73.2	328	2	I47160	Ig gamma 2b chain
12	906.5	73.2	328	2	I47159	Ig gamma 2a chain
13	903.5	73.0	277	2	I47162	Ig gamma 4 chain c

14	889	71.8	329	1	G2GP	Ig gamma-2 chain C
15	885.5	71.5	328	2	I47158	Ig gamma 1 chain c
16	878.5	71.0	328	2	I47161	Ig gamma 3 chain c
17	855.5	69.1	470	2	S22080	Ig heavy chain pre
18	846	68.3	308	2	C30554	Ig heavy chain C r
19	846	68.3	472	2	S31459	Ig gamma-1 chain -
20	845.5	68.3	329	1	G3MSC	Ig gamma-3 chain C
21	838	67.7	333	2	PS0018	Ig gamma-2b chain
22	834.5	67.4	398	1	G3MSM	Ig gamma-3 chain C
23	827.5	66.8	444	2	PC4436	monoclonal antibod
24	818.5	66.1	326	2	PS0017	Ig gamma-1 chain C
25	817.5	66.0	324	1	G1MS	Ig gamma-1 chain C
26	812.5	65.6	393	1	G1MSM	Ig gamma-1 chain C
27	809.5	65.4	329	2	S00847	Ig gamma-2c chain
28	809	65.3	330	1	G2MSA	Ig gamma-2a chain
29	809	65.3	469	2	S37483	Ig gamma-2a chain
30	804	64.9	399	1	G2MSAM	Ig gamma-2a chain
31	802	64.8	335	1	G2MSAB	Ig gamma-2a chain
32	794	64.1	446	2	S40295	Ig gamma-2a chain
33	785.5	63.4	322	2	PS0019	Ig gamma-2a chain
34	779	62.9	474	1	G2MS11	Ig gamma-2b chain
35	774	62.5	405	1	G2MSBM	Ig gamma-2b chain
36	764	61.7	327	2	S06611	Ig gamma-2 chain C
37	757	61.1	475	2	S01321	Ig gamma-2b chain
38	707	57.1	180	2	I46732	Ig gamma heavy cha
39	577.5	46.6	249	2	S69340	Ig heavy chain VHI
40	574.5	46.4	218	2	A36040	Ig heavy chain V-I
41	571	46.1	152	2	S14236	Ig gamma-1 chain C
42	395.5	31.9	572	2	B46529	Ig Y heavy chain (
43	358	28.9	343	2	S25644	Ig mu chain C regi
44	358	28.9	453	2	S37768	Ig mu chain C regi
45	357.5	28.9	549	2	S04845	Ig heavy chain pre

ALIGNMENTS

RESULT 1
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 99.6%; Score 1233; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 6.8e-89;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 88

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 208

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        209 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255
```

RESULT 2
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, 239-Asp and 241-Leu
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G.M.
Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H-1-H-4.
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequence of heavy-chain cyanogen bromide fragments H-5-H-7.
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,'M',242-267,'DGEPE',273-329 <RUT>
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie), III. Die chymotryptischen Peptide der H-Kette, Anordnung der tryptischen Peptide und Diskussion der vollstaendigen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',270-271,'D',273-330 <PON>
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL, I.
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH>
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide bonds.
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains the cyanogenbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds

C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 99.6%; Score 1233; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 9.4e-89;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 163

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 283

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        284 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

RESULT 3
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.

submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 99.1%; Score 1227; DB 2; Length 374;
Best Local Similarity 99.1%; Pred. No. 3.2e-88;
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 207

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        268 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 327

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374
```

RESULT 4
PT0207
Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 <EHR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 95.3%; Score 1180; DB 2; Length 234;
Best Local Similarity 98.6%; Pred. No. 8.2e-85;
Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              | ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         15 DTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 74

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          75 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 134

Qy         122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
               ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db         135 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTTPPVLDS 194

Qy         182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 221
               |||||||||||||||||||||||||||||||||||||||
Db         195 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 234
```

RESULT 5
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: comparison with the other human C-gamma genes.
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

```
  Query Match             92.6%;  Score 1146;  DB 2;  Length 377;
  Best Local Similarity   92.5%;  Pred. No. 6.7e-82;
  Matches  210;  Conservative    8;  Mismatches    9;  Indels    0;  Gaps    0;

Qy           2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
               |    || ||||||||||||||||||||||||||||||||||||||||||:| ||||
Db         151 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 210

Qy          62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
               ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||| |
Db         211 GVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270

Qy         122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
               ||||||||||||||:|:|||||||||||||||||||||:||||||| ||||:|||
Db         271 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 330

Qy         182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
               ||||||||||||||||||||:|||||||||||| :||||||||||
Db         331 DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK 377
```

RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 converted region and three hinge exons.
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 1144; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 9.6e-82;
Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

```
Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |    || |||||||||||||||||||||||||||||||||||||||||||:| ||||
Db        151 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 210

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||| |
Db        211 GVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||:|:|||||||||||||||||||||:||||||| ||||||||
Db        271 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPVLDS 330

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||:|||||||||:|||||||||||||||| :||||||||||
Db        331 DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNRFTQKSLSLSPGK 377
```

RESULT 7
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A;Note: Lys-326 is probably removed posttranslationally

R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-234,'Z',236-263,'BGEPZ',269-325 <CON>
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin gamma chains.
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidation states of residues 58, 194, and 197; the amidation states of residues 172-174, 176, and 235 were not determined
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.3%; Score 1142.5; DB 1; Length 326;
Best Local Similarity 94.1%; Pred. No. 1e-81;
Matches 209; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

```
Qy          7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
              ||||||| : |||||||||||||||||||||||||||||||||:||||||||||
Db        106 CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH 164

Qy         67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
              ||||||||||:|||:||||||||:|||||||||||||||| |||||||||| ||||||
Db        165 NAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPRE 224

Qy        127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 186
              ||||||||||:|:|||||||||||||||||||||||||||||||||||:||||||||
Db        225 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFF 284

Qy        187 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||
Db        285 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326
```

RESULT 8
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant region of A gamma4 chain.
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.7%; Score 1135; DB 1; Length 327;
Best Local Similarity 93.7%; Pred. No. 4e-81;
Matches 208; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

```
Qy          7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
              || ||||| |||||||||||||||||||||||||||||||||| |||||:||||||||||
Db        106 CPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH 165

Qy         67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
              ||||||||||:|||||||||||||||||||||||||||| ||: ||||||||||||||
Db        166 NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE 225

Qy        127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 186
              |||||||||::|:||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 285

Qy        187 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||:|||||||||:|||||||||||||||||||||||| ||
Db        286 LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327
```

RESULT 9
G3HUWI
Ig gamma-3 heavy chain disease proteins - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A92219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain disease protein Wis.
A;Reference number: A90442; MUID:81021548; PMID:6774747
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
A;Molecule type: protein
A;Residues: 1-289 <FRA>
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain disulfide bond at position 7 in addition to the 11 normally present in the hinge region
A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 corresponds to the beginning of the hinge region of normal gamma-3 chains

A;Note: the sequence of residues 42-76 was taken from the reference that follows
R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication of a 15-amino acid residue basic unit.
A;Reference number: A92219; MUID:77118561; PMID:402363
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein Wis
A;Accession: A92219
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma chains and contains three identical 15-residue segments (29-43, 44-58, and 59-73) preceded by a similar 17-residue segment (12-28)
A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter-heavy chain bonds
R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the Fc fragment of immunoglobulin G3.
A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues 59-289 of protein Wis
A;Accession: A90198
A;Molecule type: protein
A;Residues: 59-125,'EB',128-226,228-289 <WOL>
A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the hinge compared with normal gamma-3 heavy chains
R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.; Buxbaum, J.N.
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion model.
A;Reference number: A93915; MUID:82247835; PMID:6808505
A;Contents: heavy chain disease protein Omm
A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157,'N',159-181,'A',183-186;199-226,'N',228-278,'Y',280-289 <ALE>
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 90.5%; Score 1121; DB 1; Length 289;
Best Local Similarity 90.3%; Pred. No. 4.2e-80;
Matches 204; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

```
Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |    || |||||||||||||||||||||||||||||||||||||||||||:| ||||
Db         64 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 123

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||:||||||||||:|:|||:||||||||||:||:||||||||||||||||||||| |
Db        124 GVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              |||||||||||||||:|:||||||||||||||||||||||:||||||| ||||:|||
Db        184 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 243

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227
              ||||||||||||||||||||:||||||||||| :||||||||||
Db        244 DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG 289
```

RESULT 10
GHRB
Ig gamma chain C region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype.
A;Reference number: A91749; MUID:84030930; PMID:6313520
A;Accession: A91749
A;Molecule type: mRNA
A;Residues: 1-323 <BER>
A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R;Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.
A;Reference number: A90290; MUID:76135469; PMID:1243651
A;Accession: A90290
A;Molecule type: protein
A;Residues: 1-47,'E',49-71,'PV',72-128 <PRA>
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain and identification of two genomic C-gamma genes.
A;Reference number: A93928; MUID:83299917; PMID:6193512
A;Accession: A93928
A;Molecule type: mRNA
A;Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
A;Cross-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112
A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker, 185-Ala
R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.
A;Reference number: A90245; MUID:70110015; PMID:5461106

A;Accession: A90245
A;Molecule type: protein
A;Residues: 132-143,'E',145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, Stockholm, 1967
A;Reference number: A94416
A;Accession: A94416
A;Molecule type: protein
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',234-245,'D',247-255,'G',257-259,'D',261-265,'D',267-279,'W',281-283,'S',285-322 <HIL>
A;Note: this has the e15 allotypic marker, 185-Ala
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology <IM1>
F;130-199/Domain: immunoglobulin homology <IM2>
F;236-303/Domain: immunoglobulin homology <IM3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.2%; Score 918.5; DB 1; Length 323;
Best Local Similarity 71.7%; Pred. No. 2.9e-64;
Matches 167; Conservative 29; Mismatches 32; Indels 5; Gaps 2;

```
Qy          1 MDKT---HTC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55
              :|||    ||  | || ||||||||||:|||||||||||||||||||||| :||||:
Db         91 VDKTVAPSTCSKPTCPPPELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQ 150

Qy         56 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 115
              | ||::  :|  |:   ||:|:||| |||| | : ||||| |||:|||| ||||||||||
Db        151 FTWYINNEQVRTARPPLREQQFNSTIRVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEK 210

Qy        116 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 175
              |||||:||| ||:|||: | |:||:   |||||:: |||||||:|||| ||: |:|||||
Db        211 TISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTT 270

Qy        176 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              | |||||||:|||:||:|  | ||:|:||:||||||||||||||:| ||||
Db        271 PAVLDSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK 323
```

RESULT 11
I47160
Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single animal.
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47160

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 906.5; DB 2; Length 328;
Best Local Similarity 73.2%; Pred. No. 2.6e-63;
Matches 164; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

```
Qy          7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
              || ||| |   |||||:|||||||||||||||:|||||||| |:|||:|:|||||||||
Db        106 CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH 164

Qy         67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
              |:|:|:|||:|||||||||| : |||||||||:||||:|| ||||| : ||||||| ||
Db        165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE 224

Qy        127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGS 184
              ||||||||  :||::::||:|||| |||| || |||: |||  || ||:||||  | ||:
Db        225 PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT 284

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :||||| :|||: || | :| |:|||||||||||||:| :|||
Db        285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
```

RESULT 12
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single animal.
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 906.5; DB 2; Length 328;
Best Local Similarity 73.2%; Pred. No. 2.6e-63;
Matches 164; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

```
Qy          7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
              || ||| |   |||||:|||||||||||||||:|||||||| |:|||:|:|||||||||
```

```
Db        106 CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH 164

Qy         67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
              |:|:|:|||:|||||||||| : |||||||||:||||:|| ||||| : ||||||| ||
Db        165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE 224

Qy        127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGS 184
              |||||||| :||::::||:|||| |||| || |||: ||| || ||:|||| | ||:
Db        225 PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT 284

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :||||| :|||: || | :| |:||||||||||||||:| :|||
Db        285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328


RESULT 13
I47162
Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA
sequences of a single animal.
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47162
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>

  Query Match             73.0%;  Score 903.5;  DB 2;  Length 277;
  Best Local Similarity   71.1%;  Pred. No. 3.6e-63;
  Matches  167;  Conservative   30;  Mismatches   31;  Indels    7;  Gaps    4;

Qy          1 MDK---THTCPPCP-APELLG-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55
              :||   | | ||||  |   | ||| |:||||||||||||||:||||||||| |:|||:
Db         43 VDKRVGTKTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQ 102

Qy         56 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 115
              |:||||||||| |:|:|:|||:|||||||||| : |||||||||:||||:|| ||||| :
Db        103 FSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITR 162

Qy        116 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYK 173
              ||||||| |||||||||| :||::::|:||||| |||| || |||: ||| || ||:
Db        163 IISKAKGQTREPQVYTLPPPTEELSRSKVTLTCLVTGFYPPDIDVEWQRNGQPEPEGNYR 222

Qy        174 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||| | ||::|||||| |||: ||:|: | |:||||||||||||||:  :|||
Db        223 TTPPQQDVDGTYFLYSKLAVDKASWQRGDTFQCAVMHEALHNHYTQKSIFKTPGK 277
```

RESULT 14
G2GP
Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151
R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
A;Accession: A94553
A;Molecule type: protein
A;Residues: 1-3 <TRI>
R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Amino acid sequence of the region around the half-cystine joining heavy and light chains.
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
A;Molecule type: protein
A;Residues: 4-68 <BIR>
R;Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal and hinge region cyanogen bromide fragments.
A;Reference number: A90359; MUID:71058486; PMID:5538616
A;Accession: A90359
A;Molecule type: protein
A;Residues: 69-133;312-329 <TUR>
R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90384; MUID:75036072; PMID:4429665
A;Accession: A90384
A;Molecule type: protein
A;Residues: 134-226 <TRA>
R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
A;Molecule type: protein
A;Residues: 227-311 <TR2>
R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A;Reference number: A90354; MUID:71058474; PMID:4922544
A;Contents: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma,

```
or mu) chains usually stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;21-81/Domain: immunoglobulin homology <IM1>
F;135-204/Domain: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
F;142-202/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental

  Query Match             71.8%;  Score 889;  DB 1;  Length 329;
  Best Local Similarity   72.3%;  Pred. No. 6e-62;
  Matches  162;  Conservative   24;  Mismatches   36;  Indels    2;  Gaps    1;

Qy          6 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65
              ||| || || |||||||:||||||||||||| || ||||||||| ::|||:| |:||   |
Db        106 TCPKCPPPENLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPV 165

Qy         66 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
              ||:|||| |||||:|:|| ||| : ||||| |||:|||| |||||||||||||| || ||
Db        166 GNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPR 225

Qy        126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDG 183
              | |||||||||||:|::||:|||:  |:|:|| ||| ||  |  |  || |||: |:||
Db        226 MPDVYTLPPSRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADG 285

Qy        184 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227
              |:|||||||||| | || |::|||||||||| |||::| |||
Db        286 SYFLYSKLTVDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329


RESULT 15
I47158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA
sequences of a single animal.
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C;Genetics:
A;Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             71.5%;  Score 885.5;  DB 2;  Length 328;
  Best Local Similarity   72.4%;  Pred. No. 1.1e-61;
  Matches  163;  Conservative   27;  Mismatches   32;  Indels    3;  Gaps    2;
```

```
Qy          6 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65
              ||| ||  | : |||||:||||||||||||:||||||||||||| |  ||:|:||||||||
Db        105 TCPICPGCE-VAGPSVFIFPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEV 163

Qy         66 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
              | |:|:|:|||:|||||||||| : ||||| |||:||||:|  ||||| :||||| || |
Db        164 HTAETRPKEEQFNSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSR 223

Qy        126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDG 183
              |||||||||  :||::::|:||||| |||| || |||:||||  ||| |:||||  | ||
Db        224 EPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDG 283

Qy        184 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :|||||| |||:||  |: | |:||||||||||||||:| : ||
Db        284 TFFLYSKLAVDKARWDHGDKFECAVMHEALHNHYTQKSISKTQGK 328
```

Search completed: January 16, 2004, 15:58:59
Job time : 21 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 16, 2004, 15:53:55 ; Search time 18 Seconds
(without alignments)
595.672 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1233	99.6	330	1	GC1_HUMAN	P01857 homo sapien
2	1142.5	92.3	326	1	GC2_HUMAN	P01859 homo sapien
3	1135	91.7	327	1	GC4_HUMAN	P01861 homo sapien
4	1126	91.0	290	1	GC3_HUMAN	P01860 homo sapien
5	918.5	74.2	323	1	GC_RABIT	P01870 oryctolagus
6	889	71.8	329	1	GC2_CAVPO	P01862 cavia porce
7	845.5	68.3	329	1	GC3_MOUSE	P22436 mus musculu
8	838	67.7	333	1	GCB_RAT	P20761 rattus norv
9	834.5	67.4	398	1	GC3M_MOUSE	P03987 mus musculu
10	818.5	66.1	326	1	GC1_RAT	P20759 rattus norv
11	817.5	66.0	324	1	GC1_MOUSE	P01868 mus musculu
12	812.5	65.6	393	1	GC1M_MOUSE	P01869 mus musculu
13	809.5	65.4	329	1	GCC_RAT	P20762 rattus norv
14	809	65.3	330	1	GCAA_MOUSE	P01863 mus musculu
15	804	64.9	399	1	GCAM_MOUSE	P01865 mus musculu
16	802	64.8	335	1	GCAB_MOUSE	P01864 mus musculu
17	785.5	63.4	322	1	GCA_RAT	P20760 rattus norv

18	779	62.9	336	1	GCB_MOUSE	P01866 mus musculu
19	774	62.5	405	1	GCBM_MOUSE	P01867 mus musculu
20	358	28.9	454	1	MUC_HUMAN	P01871 homo sapien
21	357	28.8	455	1	MUC_MOUSE	P01872 mus musculu
22	356	28.8	391	1	MUCB_HUMAN	P04220 homo sapien
23	354	28.6	421	1	EPC_MOUSE	P06336 mus musculu
24	353	28.5	429	1	EPC_RAT	P01855 rattus norv
25	352	28.4	428	1	EPC_HUMAN	P01854 homo sapien
26	347	28.0	476	1	MUCM_MOUSE	P01873 mus musculu
27	342	27.6	458	1	MUC_RABIT	P03988 oryctolagus
28	332	26.8	450	1	MUC_CANFA	P01874 canis famil
29	332	26.8	454	1	MUC_MESAU	P06337 mesocricetu
30	332	26.8	479	1	MUCM_RABIT	P04221 oryctolagus
31	329	26.6	457	1	MUC_SUNMU	P20768 suncus muri
32	297	24.0	438	1	HVC2_HETFR	P23085 heterodontu
33	295.5	23.9	299	1	ALC_RABIT	P01879 oryctolagus
34	287.5	23.2	438	1	HVCS_HETFR	P23087 heterodontu
35	287.5	23.2	446	1	MUC_CHICK	P01875 gallus gall
36	278.5	22.5	461	1	HVCM_HETFR	P23088 heterodontu
37	276.5	22.3	393	1	HVC3_HETFR	P23086 heterodontu
38	272	22.0	353	1	ALC1_HUMAN	P01876 homo sapien
39	272	22.0	370	1	HVC1_HETFR	P23084 heterodontu
40	267.5	21.6	353	1	ALC1_GORGO	P20758 gorilla gor
41	267	21.6	340	1	ALC2_HUMAN	P01877 homo sapien
42	248.5	20.1	481	1	MUCM_ICTPU	P23735 ictalurus p
43	245	19.8	344	1	ALC_MOUSE	P01878 mus musculu
44	179	14.5	513	1	SHS1_MOUSE	P97797 m protein-t
45	177.5	14.3	105	1	LAC1_MOUSE	P01843 mus musculu

ALIGNMENTS

```
RESULT 1
GC1_HUMAN
ID   GC1_HUMAN      STANDARD;      PRT;   330 AA.
AC   P01857;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-1 chain C region.
GN   IGHG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82274238; PubMed=6287432;
RA   Ellison J.W., Berson B.J., Hood L.E.;
RT   "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL   Nucleic Acids Res. 10:4071-4079(1982).
RN   [2]
RP   SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA   Waxdal M.J., Edelman G.M.;
```

```
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [3]
RP   SEQUENCE OF 136-329 (EU).
RX   MEDLINE=71064025; PubMed=5530842;
RA   Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA   Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL   Biochemistry 9:3171-3181(1970).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN NIE).
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [5]
RP   SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981).
CC   -!- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
CC       G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
CC       MARKER & THE G1M (NON-1) MARKERS.
CC   -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC       35,116,198,269 & 272.
CC   -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
```

```
CC       155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC       268-272.
CC   -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC       RESIDUES 198,267&272.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A93433; GHHU.
DR   PDB; 1FC1; 15-JUL-92.
DR   PDB; 1FC2; 15-JUL-92.
DR   PDB; 1AJ7; 12-NOV-97.
DR   PDB; 1D5B; 09-FEB-00.
DR   PDB; 1D5I; 09-FEB-00.
DR   PDB; 1D6V; 04-OCT-00.
DR   PDB; 1DN2; 17-MAY-00.
DR   PDB; 1E4K; 06-JUN-01.
DR   PDB; 1FCC; 20-JUL-95.
DR   PDB; 1HZH; 12-JUN-02.
DR   PDB; 1I7Z; 08-AUG-01.
DR   PDB; 1IIS; 16-MAY-01.
DR   PDB; 1IIX; 16-MAY-01.
DR   PDB; 1L6X; 10-APR-02.
DR   PDB; 2RCS; 12-NOV-97.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding activity; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    223       CH2.
FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    103       INTERCHAIN (WITH LIGHT CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .).
FT   MOD_RES     330    330       REMOVED POST-TRANSLATIONALLY.
```

```
FT   VARIANT      97     97       K -> R (IN G1M(3) MARKER).
FT                                /FTId=VAR_003886.
FT   VARIANT     239    239       D -> E (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003887.
FT   VARIANT     241    241       L -> M (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003888.
FT   STRAND      122    126
FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    147
FT   STRAND      157    162
FT   TURN        163    164
FT   STRAND      165    166
FT   TURN        168    171
FT   STRAND      176    179
FT   TURN        180    181
FT   STRAND      182    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    207
FT   TURN        209    210
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    242
FT   STRAND      245    256
FT   STRAND      260    265
FT   STRAND      270    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      305    312
FT   TURN        313    314
FT   TURN        316    317
FT   STRAND      320    325
SQ   SEQUENCE   330 AA;  36106 MW;  3770EE106C2FA33D CRC64;

  Query Match             99.6%;  Score 1233;  DB 1;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-93;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 163

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 283

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 2
GC2_HUMAN
ID   GC2_HUMAN      STANDARD;      PRT;   326 AA.
AC   P01859;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-2 chain C region.
GN   IGHG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 2-326 FROM N.A.
RX   MEDLINE=82197621; PubMed=6804948;
RA   Ellison J.W., Hood L.E.;
RT   "Linkage and sequence homology of two human immunoglobulin gamma
RT   heavy chain constant region genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN   [2]
RP   SEQUENCE OF 88-115 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=83001943; PubMed=6811139;
RA   Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT   "Structure of human immunoglobulin gamma genes: implications for
RT   evolution of a gene family.";
RL   Cell 29:671-679(1982).
RN   [3]
RP   SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=84235992; PubMed=6329676;
RA   Krawinkel U., Rabbitts T.H.;
RT   "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT   heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT   genes.";
RL   EMBO J. 1:403-407(1982).
RN   [4]
RP   SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX   MEDLINE=81007873; PubMed=6774012;
RA   Wang A.-C., Tung E., Fudenberg H.H.;
RT   "The primary structure of a human IgG2 heavy chain: genetic,
RT   evolutionary, and functional implications.";
RL   J. Immunol. 125:1048-1054(1980).
RN   [5]
RP   SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX   MEDLINE=80001357; PubMed=113060;
RA   Connell G.E., Parr D.M., Hofmann T.;
RT   "The amino acid sequences of the three heavy chain constant region
RT   domains of a human IgG2 myeloma protein.";
RL   Can. J. Biochem. 57:758-767(1979).
RN   [6]
RP   SEQUENCE OF 238-275 (ZIE).
```

```
RX   MEDLINE=80114419; PubMed=118920;
RA   Hofmann T., Parr D.M.;
RT   "A note of the amino acid sequence of residues 381-391 of human
RT   immunoglobulins gamma chains.";
RL   Mol. Immunol. 16:923-925(1979).
RN   [7]
RP   REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA   Hofmann T., Parr D.M.;
RL   Submitted (MAR-1980) to the PIR data bank.
RN   [8]
RP   SEQUENCE OF 1-121 (DOT).
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE=72033500; PubMed=4940472;
RA   Milstein C., Frangione B.;
RT   "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL   Biochem. J. 121:217-225(1971).
RN   [10]
RP   DISULFIDE BONDS.
RX   MEDLINE=69064124; PubMed=5782707;
RA   Frangione B., Milstein C., Pink J.R.L.;
RT   "Structural studies of immunoglobulin G.";
RL   Nature 221:145-148(1969).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00230; AAB59393.1; -.
DR   PIR; A93906; G2HU.
DR   HSSP; P01857; 1FC1.
DR   Genew; HGNC:5526; IGHG2.
DR   MIM; 147110; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding activity; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    219       CH2.
```

```
FT   DOMAIN       220     326       CH3.
FT   DISULFID      14      14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID      27      83
FT   DISULFID     102     102       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID     103     103       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID     106     106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID     109     109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID     140     200
FT   DISULFID     246     304
FT   SITE         156     156       AT OR NEAR THE COMPLEMENT-BINDING SITE.
FT   MOD_RES      326     326       REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT   VARIANT       60      60       S -> A (IN MYELOMA PROTEINS TIL & ZIE).
FT                                  /FTId=VAR_003889.
FT   CONFLICT     109     109       C -> S (IN REF. 3).
SQ   SEQUENCE   326 AA;  35884 MW;  8310878C6878CF9C CRC64;

  Query Match             92.3%;  Score 1142.5;  DB 1;  Length 326;
  Best Local Similarity   94.1%;  Pred. No. 5e-86;
  Matches  209;  Conservative    8;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
              ||||||| : |||||||||||||||||||||||||||||||||||:||||||||||
Db        106 CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH 164

Qy         67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
              |||||||||:|||:||||||||:|||||||||||||||| |||||||||| ||||||
Db        165 NAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPRE 224

Qy        127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 186
              ||||||||||:|:|||||||||||||||||||||||||||||||||||:||||||||
Db        225 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFF 284

Qy        187 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||
Db        285 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326


RESULT 3
GC4_HUMAN
ID   GC4_HUMAN      STANDARD;      PRT;   327 AA.
AC   P01861;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-4 chain C region.
GN   IGHG4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83157104; PubMed=6299662;
RA   Ellison J.W., Buxbaum J.N., Hood L.E.;
RT   "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL   DNA 1:11-18(1981).
RN   [2]
```

```
RP   SEQUENCE OF 1-30 AND 81-326.
RX   MEDLINE=70207560; PubMed=4192699;
RA   Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT   "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT   constant region of a gamma 4 chain.";
RL   Biochem. J. 117:33-47(1970).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K01316; AAB59394.1; ALT_INIT.
DR   PIR; A90933; G4HU.
DR   PDB; 1ADQ; 16-SEP-98.
DR   Genew; HGNC:5528; IGHG4.
DR   MIM; 147130; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding activity; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    220       CH2.
FT   DOMAIN      221    327       CH3.
FT   DISULFID     14     14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     83
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    141    201
FT   DISULFID    247    305
SQ   SEQUENCE   327 AA;  35940 MW;  3EDBD811EF208E7A CRC64;

  Query Match             91.7%;  Score 1135;  DB 1;  Length 327;
  Best Local Similarity   93.7%;  Pred. No. 2.1e-85;
  Matches  208;  Conservative    8;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
              || ||||| |||||||||||||||||||||||||||||||| |||||:||||||||||||
Db        106 CPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH 165

Qy         67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
              ||||||||||:|||||||||||||||||||||||||||| ||: ||||||||||||||
Db        166 NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE 225

Qy        127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 186
```

```
                ||||||||::|:||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 285

Qy        187 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                |||:||||||||:|||||||||||||||||||||||| ||
Db        286 LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327


RESULT 4
GC3_HUMAN
ID   GC3_HUMAN      STANDARD;      PRT;   290 AA.
AC   P01860;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN   IGHG3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (DISEASE PROTEIN WIS).
RX   MEDLINE=81021548; PubMed=6774747;
RA   Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT   "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RT   gamma 3 heavy-chain disease protein Wis.";
RL   Biochemistry 19:4304-4308(1980).
RN   [2]
RP   REVISIONS TO 12-97 (PROTEIN WIS).
RX   MEDLINE=77118561; PubMed=402363;
RA   Michaelsen T.E., Frangione B., Franklin E.C.;
RT   "Primary structure of the 'hinge' region of human IgG3. Probable
RT   quadruplication of a 15-amino acid residue basic unit.";
RL   J. Biol. Chem. 252:883-889(1977).
RN   [3]
RP   REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX   MEDLINE=77021516; PubMed=823945;
RA   Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT   "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT   Structure of the Fc fragment of immunoglobulin G3.";
RL   Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN   [4]
RP   SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX   MEDLINE=82247835; PubMed=6808505;
RA   Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA   Franklin E.C., Hood L., Buxbaum J.N.;
RT   "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT   gene deletion model.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC   -!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC       INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC       NORMALLY PRESENT IN THE HINGE REGION.
CC   -!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC   -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC       REF.2.
CC   -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
```

```
CC       AND ALL OF THE CH1 REGION.
CC   -!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CC       OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
CC       GAMMA-3 HEAVY CHAINS.
CC   -!- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
CC       OR ANOTHER GAMMA CHAIN SUBCLASS.
CC   -!- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
CC       TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
CC       IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
CC       SEGMENT (12-28).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00231; AAA52805.1; ALT_SEQ.
DR   HSSP; P01857; 1FC1.
DR   Genew; HGNC:5527; IGHG3.
DR   MIM; 147120; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding activity; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN       12     73       HINGE.
FT   DOMAIN       74    183       CH2.
FT   DOMAIN      184    289       CH3.
FT   REPEAT       29     43
FT   REPEAT       44     58
FT   REPEAT       59     73
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   CARBOHYD      6      6       N-LINKED (GLCNAC. . .).
FT   DISULFID      7      7       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     24     24       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     27     27       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     33     33       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     39     39       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     42     42       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     48     48       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     54     54       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     57     57       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     63     63       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     69     69       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     72     72       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   CARBOHYD    140    140       N-LINKED (GLCNAC. . .).
FT   MOD_RES     290    290       REMOVED POST-TRANSLATIONALLY.
```

```
FT   VARIANT      126     127       QV -> EB (IN ZUC).
FT                                  /FTId=VAR_003890.
FT   VARIANT      134     134       P -> L (IN OMM).
FT                                  /FTId=VAR_003891.
FT   VARIANT      139     139       F -> Y (IN OMM).
FT                                  /FTId=VAR_003892.
FT   VARIANT      182     182       T -> A (IN OMM).
FT                                  /FTId=VAR_003893.
FT   VARIANT      227     227       S -> N (IN OMM).
FT                                  /FTId=VAR_003894.
FT   VARIANT      227     227       MISSING (IN ZUC).
FT                                  /FTId=VAR_003895.
FT   VARIANT      279     279       F -> Y (IN OMM).
FT                                  /FTId=VAR_003896.
SQ   SEQUENCE   290 AA;  32331 MW;  E69CBC95705B2F46 CRC64;

  Query Match             91.0%;  Score 1126;  DB 1;  Length 290;
  Best Local Similarity   90.3%;  Pred. No. 9.6e-85;
  Matches  205;  Conservative   13;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |    || |||||||||||||||||||||||||||||||||||||||||||:| ||||
Db         64 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 123

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||:|||||||||:|:|||:||||||||||:||:|||||||||||||||||||| |
Db        124 GVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||:|:|||||||||||||||||||||:||||||| ||||:|||
Db        184 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 243

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||:||||||||||| :||||||||||
Db        244 DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK 290


RESULT 5
GC_RABIT
ID   GC_RABIT       STANDARD;      PRT;   323 AA.
AC   P01870;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig gamma chain C region.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84030930; PubMed=6313520;
RA   Bernstein K.E., Alexander C.B., Mage R.G.;
RT   "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT   F-I haplotype.";
RL   Immunogenetics 18:387-397(1983).
RN   [2]
```

```
RP   SEQUENCE OF 1-128.
RX   MEDLINE=76135469; PubMed=1243651;
RA   Pratt D.M., Mole L.E.;
RT   "Sequence studies on the constant region of the Fd sections of rabbit
RT   immunoglobulin G of different allotype.";
RL   Biochem. J. 151:337-349(1975).
RN   [3]
RP   SEQUENCE OF 88-266 FROM N.A.
RX   MEDLINE=83299917; PubMed=6193512;
RA   Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT   "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT   heavy chain and identification of two genomic C gamma genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN   [4]
RP   SEQUENCE OF 132-161.
RX   MEDLINE=70110015; PubMed=5461106;
RA   Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT   "Sequence studies of the Fd section of the heavy chain of rabbit
RT   immunoglobulin G.";
RL   Biochem. J. 116:249-259(1970).
RN   [5]
RP   SEQUENCE OF 129-131 AND 155-322.
RA   Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL   (In) Killander J. (eds.);
RL   Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL   Stockholm (1967).
CC   -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC       104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC       MARKERS AND REF.5 THE E15 MARKER.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M16426; AAA31289.1; -.
DR   PIR; A91749; GHRB.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     96       IG-LIKE 1.
FT   DOMAIN      114    213       IG-LIKE 2.
FT   DOMAIN      222    318       IG-LIKE 3.
FT   VARIANT     104    104       T -> M (IN D11 MARKER).
FT   VARIANT     185    185       T -> A (IN E15 MARKER).
FT   CONFLICT     48     48       N -> E (IN REF. 2).
```

```
FT   CONFLICT     71      71       V -> VPV (IN REF. 2).
FT   CONFLICT    144     144       Q -> E (IN REF. 3 AND 4).
FT   CONFLICT    173     173       N -> D (IN REF. 5).
FT   CONFLICT    187     187       Q -> E (IN REF. 3 AND 5).
FT   CONFLICT    201     201       N -> D (IN REF. 5).
FT   CONFLICT    218     218       Q -> E (IN REF. 5).
FT   CONFLICT    233     233       E -> Q (IN REF. 5).
FT   CONFLICT    246     246       N -> D (IN REF. 5).
FT   CONFLICT    256     256       E -> G (IN REF. 5).
FT   CONFLICT    260     260       N -> D (IN REF. 5).
FT   CONFLICT    266     266       N -> D (IN REF. 5).
FT   CONFLICT    280     280       Y -> W (IN REF. 5).
FT   CONFLICT    284     284       N -> S (IN REF. 5).
SQ   SEQUENCE   323 AA;  35404 MW;  69E8AA118D579A8B CRC64;

  Query Match             74.2%;  Score 918.5;  DB 1;  Length 323;
  Best Local Similarity   71.7%;  Pred. No. 8.9e-68;
  Matches  167;  Conservative   29;  Mismatches   32;  Indels    5;  Gaps    2;

Qy          1 MDKT---HTC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55
              :|||    ||  | || ||||||||||:||||||||||||||||||||||||| :||||:
Db         91 VDKTVAPSTCSKPTCPPPELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQ 150

Qy         56 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 115
              | ||::  :|  |:   ||:|:||| |||| | : ||||| |||:|||| ||||||||||
Db        151 FTWYINNEQVRTARPPLREQQFNSTIRVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEK 210

Qy        116 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 175
              |||||:||| ||:|||: | |:||:   |||||:: |||||||:|||| ||: |:|||||
Db        211 TISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTT 270

Qy        176 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              | |||||||:|||:||:|  | ||:|:||:||||||||||||||:| ||||
Db        271 PAVLDSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK 323


RESULT 6
GC2_CAVPO
ID   GC2_CAVPO      STANDARD;      PRT;   329 AA.
AC   P01862;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2 chain C region.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE OF 1-3.
RA   Trischmann T.M.;
RL   Submitted (APR-1975) to the PIR data bank.
RN   [2]
RP   SEQUENCE OF 4-68.
RX   MEDLINE=71058471; PubMed=5538606;
RA   Birshtein B.K., Hussain Q.Z., Cebra J.J.;
RT   "Structure of heavy chain from strain 13 guinea pig
```

```
RT   immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT   half-cystine joining heavy and light chains.";
RL   Biochemistry 10:18-25(1971).
RN   [3]
RP   SEQUENCE OF 69-133 AND 312-329.
RX   MEDLINE=71058486; PubMed=5538616;
RA   Turner K.J., Cebra J.J.;
RT   "Structure of heavy chain from strain 13 guinea pig
RT   immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT   and hinge region cyanogen bromide fragments.";
RL   Biochemistry 10:9-17(1971).
RN   [4]
RP   SEQUENCE OF 134-226.
RX   MEDLINE=75036072; PubMed=4429665;
RA   Tracey D.E., Cebra J.J.;
RT   "Primary structure of the CH2 homology region from guinea pig IgG2
RT   antibodies.";
RL   Biochemistry 13:4796-4803(1974).
RN   [5]
RP   SEQUENCE OF 227-311.
RX   MEDLINE=75036073; PubMed=4609467;
RA   Trischmann T.M., Cebra J.J.;
RT   "Primary structure of the CH3 homology region from guinea pig IgG2
RT   antibodies.";
RL   Biochemistry 13:4804-4811(1974).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71058474; PubMed=4922544;
RA   Oliveira B., Lamm M.E.;
RT   "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL   Biochemistry 10:26-31(1971).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC       13 INBRED GUINEA PIGS.
DR   PIR; A94553; G2GP.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT   NON_TER       1      1
FT   DISULFID     16     16       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     28     79
FT   DISULFID    105    105       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    110    110       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    142    202
FT   CARBOHYD    178    178       N-LINKED (GLCNAC. . .).
FT   DISULFID    248    308
SQ   SEQUENCE   329 AA;  36074 MW;  5D231B7164D1FBA9 CRC64;

  Query Match             71.8%;  Score 889;  DB 1;  Length 329;
  Best Local Similarity   72.3%;  Pred. No. 2.3e-65;
  Matches  162;  Conservative   24;  Mismatches   36;  Indels    2;  Gaps    1;
```

```
Qy          6 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65
              ||| || || |||||||:|||||||||||| || ||||||||| ::|||:| |:||   |
Db        106 TCPKCPPPENLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPV 165

Qy         66 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
              ||:|||| |||||:|:|| ||| : ||||| |||:|||| |||||||||||||| || ||
Db        166 GNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPR 225

Qy        126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDG 183
              | |||||||||||:|::||:|||:  |:|:|| ||| ||  |  |  || |||: |:||
Db        226 MPDVYTLPPSRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADG 285

Qy        184 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227
              |:||||||||||| | || |::|||||||||| |||::| |||
Db        286 SYFLYSKLTVDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
```

```
RESULT 7
GC3_MOUSE
ID   GC3_MOUSE      STANDARD;      PRT;   329 AA.
AC   P22436;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-3 chain C region, secreted form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85027161; PubMed=6092053;
RA   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA   Tucker P.W., Blattner F.R.;
RT   "Structural analysis of the murine IgG3 constant region gene.";
RL   EMBO J. 3:2041-2046(1984).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR   PIR; B02156; G3MSC.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
```

```
KW   Transmembrane; Alternative splicing.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    113       HINGE.
FT   DOMAIN      114    223       CH2.
FT   DOMAIN      224    327       CH3.
SQ   SEQUENCE   329 AA;  36228 MW;  F45827174182BAD6 CRC64;

  Query Match             68.3%;  Score 845.5;  DB 1;  Length 329;
  Best Local Similarity   67.0%;  Pred. No. 8.1e-62;
  Matches  150;  Conservative   34;  Mismatches   37;  Indels    3;  Gaps    1;

Qy          8 PP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              ||   ||   :|||||||:|||||||  ||||  ||:|||||||||  :||:|  :|:||  |
Db        106 PPGSSCPPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKE 165

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              || | |:||| |||||:|||| | : ||||: |||:||||:||||||||||:|||| ||:
Db        166 VHTAWTQPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRA 225

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
              : |||||:|| |::::| :|||||||  |:   |:|||| ||: | :|| |||:|||||:
Db        226 QTPQVYTIPPPREQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGT 285

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :|||||||||   | || :|:|||:|||||||:|||:|| ||||
Db        286 YFLYSKLTVDTDSWLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329


RESULT 8
GCB_RAT
ID   GCB_RAT        STANDARD;      PRT;   333 AA.
AC   P20761;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-2B chain C region.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89232738; PubMed=3149946;
RA   Brueggemann M.;
RT   "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL   Gene 74:473-482(1988).
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR   PIR; PS0018; PS0018.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
```

```
KW   Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     96       IG-LIKE 1.
FT   DOMAIN      124    223       IG-LIKE 2.
FT   DOMAIN      232    328       IG-LIKE 3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     80
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    115    115       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    147    207
FT   DISULFID    253    311
SQ   SEQUENCE   333 AA;  36497 MW;  55F8B64D48D460A6 CRC64;

  Query Match             67.7%;  Score 838;  DB 1;  Length 333;
  Best Local Similarity   66.4%;  Pred. No. 3.3e-61;
  Matches  148;  Conservative   33;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          6 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65
              ||  || ||||||||||:||||||| |:||:  :||||||||| |:|:|:|:|:|: |||
Db        111 TCHKCPVPELLGGPSVFIFPPKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWFVNNVEV 170

Qy         66 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
              | |:|:|||||||||:|||| | : ||||::|||:||||:|||||:|||||||| ||  |
Db        171 HTAQTQPREEQYNSTFRVVSALPIQHQDWMSGKEFKCKVNNKALPSPIEKTISKPKGLVR 230

Qy        126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 185
              :|||| : |  ::||:  ||||||  || |:|| ||| |||  | ||| | ||:||||||
Db        231 KPQVYVMGPPTEQLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMDSDGSF 290

Qy        186 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |:|||| |::|||     | |||:|| ||||: :||:|  |||
Db        291 FMYSKLNVERSRWDSRAPFVCSVVHEGLHNHHVEKSISRPPGK 333


RESULT 9
GC3M_MOUSE
ID   GC3M_MOUSE     STANDARD;      PRT;   398 AA.
AC   P03987;
DT   23-OCT-1986 (Rel. 02, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-3 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85027161; PubMed=6092053;
RA   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA   Tucker P.W., Blattner F.R.;
RT   "Structural analysis of the murine IgG3 constant region gene.";
RL   EMBO J. 3:2041-2046(1984).
RN   [2]
RP   SEQUENCE OF 328-398 FROM N.A.
```

```
RX   MEDLINE=84041483; PubMed=6314258;
RA   Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA   Wall R.;
RT   "The structure of the mouse immunoglobulin in gamma 3 membrane gene
RT   segment.";
RL   Nucleic Acids Res. 11:6775-6785(1983).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00451; AAB59655.1; -.
DR   EMBL; V01526; CAA24767.1; ALT_SEQ.
DR   PIR; A02156; G3MSM.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    113       HINGE.
FT   DOMAIN      114    223       CH2.
FT   DOMAIN      224    327       CH3.
FT   TRANSMEM    346    362       POTENTIAL.
FT   DOMAIN      363    398       CYTOPLASMIC (POTENTIAL).
FT   CONFLICT    333    333       E -> G (IN REF. 2).
FT   CONFLICT    342    342       E -> Q (IN REF. 2).
FT   CONFLICT    388    388       P -> F (IN REF. 2).
SQ   SEQUENCE   398 AA;  43929 MW;  CF7F264B50A41B95 CRC64;

  Query Match             67.4%;  Score 834.5;  DB 1;  Length 398;
  Best Local Similarity   66.7%;  Pred. No. 8e-61;
  Matches  148;  Conservative   34;  Mismatches   37;  Indels    3;  Gaps    1;

Qy          8 PP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              ||   ||   :|||||||:|||||| |||| ||:||||||||| :||:|  :|:||  |
Db        106 PPGSSCPPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKE 165

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              || | |:||| |||||:|||| | : ||||: |||:||||:||||||||||:|||| ||:
Db        166 VHTAWTQPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRA 225

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
              : |||||:|| |:::::| :|||||||  |:   |:|||| ||: | :|| |||:|||||:.
Db        226 QTPQVYTIPPPREQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGT 285

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 226
```

```
                :|||||||||    | || :|:|||:|||||||:|||:|| ||
Db        286 YFLYSKLTVDTDSWLQGEIFTCSVVHEALHNHHTQKNLSRSP 327


RESULT 10
GC1_RAT
ID   GC1_RAT        STANDARD;      PRT;   326 AA.
AC   P20759;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-1 chain C region.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89232738; PubMed=3149946;
RA   Brueggemann M.;
RT   "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL   Gene 74:473-482(1988).
DR   PIR; PS0017; PS0017.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    112       HINGE.
FT   DOMAIN      113    219       CH2.
FT   DOMAIN      220    326       CH3.
FT   DISULFID     27     82
FT   DISULFID    102    102       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    111    111       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    140    200
FT   DISULFID    246    304
FT   CARBOHYD    176    176       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   326 AA;  35946 MW;  013BAB45EF49B9DA CRC64;

  Query Match             66.1%;  Score 818.5;  DB 1;  Length 326;
  Best Local Similarity   63.1%;  Pred. No. 1.3e-59;
  Matches  142;  Conservative   41;  Mismatches   35;  Indels    7;  Gaps    2;

Qy          7 CPPCPAPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 63
              | ||    :  |    |||:||||||| | |: ||:|||||||:| :|||| |:|:|| |
Db        106 CKPC----ICTGSEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISQDDPEVHFSWFVDDV 161

Qy         64 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 123
              ||| |:|:| |||:|||:| || | :||||||||: ::|||:: | |:|||||||| :|:
```

```
Db        162 EVHTAQTRPPEEQFNSTFRSVSELPILHQDWLNGRTFRCKVTSAAFPSPIEKTISKPEGR 221

Qy        124 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 183
              : | |||: |:::|:|:|:||:||:|||||| || |||: ||||: ||| ||| :|:||
Db        222 TQVPHVYTMSPTKEEMTQNEVSITCMVKGFYPPDIYVEWQMNGQPQENYKNTPPTMDTDG 281

Qy        184 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |:|||||| | | :||||| |:|||:|| ||||:|:|||| ||||
Db        282 SYFLYSKLNVKKEKWQQGNTFTCSVLHEGLHNHHTEKSLSHSPGK 326


RESULT 11
GC1_MOUSE
ID   GC1_MOUSE      STANDARD;      PRT;   324 AA.
AC   P01868;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-1 chain C region secreted form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80045036; PubMed=115593;
RA   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA   Takahashi N., Mano Y.;
RT   "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT   gamma 1 chain gene.";
RL   Cell 18:559-568(1979).
RN   [2]
RP   SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX   MEDLINE=80202559; PubMed=6769752;
RA   Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA   Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT   "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT   cloned in a bacterial plasmid.";
RL   Gene 9:87-97(1980).
RN   [3]
RP   SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX   MEDLINE=80012837; PubMed=113776;
RA   Rogers J., Clarke P., Salser W.;
RT   "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT   heavy chain.";
RL   Nucleic Acids Res. 6:3305-3321(1979).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX   MEDLINE=78242288; PubMed=98524;
RA   Adetugbo K.;
RT   "Evolution of immunoglobulin subclasses. Primary structure of a
RT   murine myeloma gamma1 chain.";
RL   J. Biol. Chem. 253:6068-6075(1978).
RN   [5]
RP   DISULFIDE BONDS (MOPC 21).
RX   MEDLINE=73008889; PubMed=5073237;
RA   Svasti J., Milstein C.;
```

```
RT   "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL   Biochem. J. 126:837-850(1972).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Secreted;
CC         IsoId=P01868-1; Sequence=Displayed;
CC         Note=May be the major isoform;
CC       Name=Membrane-bound;
CC         IsoId=P01869-1; Sequence=External;
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00793; CAA24172.1; -.
DR   EMBL; V00793; CAA24173.1; -.
DR   EMBL; V00793; CAA24174.1; -.
DR   EMBL; V00793; CAA24175.1; -.
DR   EMBL; V00795; CAA24176.1; -.
DR   PIR; A02159; G1MS.
DR   PDB; 1IGC; 03-JUN-95.
DR   GlycoSuiteDB; P01868; -.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Alternative splicing; 3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    110       HINGE.
FT   DOMAIN      111    217       CH2.
FT   DOMAIN      218    324       CH3.
FT   DISULFID     27     82
FT   DISULFID    102    102       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID    104    104       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    138    198
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000055.
FT   DISULFID    244    302
FT   MOD_RES     324    324       REMOVED POST-TRANSLATIONALLY.
FT   CONFLICT    276    276       N -> D (IN REF. 3).
FT   CONFLICT    278    278       N -> D (IN REF. 3).
SQ   SEQUENCE   324 AA;  35704 MW;  A338812F3D1F2C93 CRC64;
```

Query Match 66.0%; Score 817.5; DB 1; Length 324;

```
  Best Local Similarity   62.5%;  Pred. No. 1.5e-59;
  Matches  140;  Conservative   44;  Mismatches   35;  Indels    5;  Gaps    2;

Qy          7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              | |  |  ||:    |||:||||||| | |: ||:|||||||:| :||||:|:|:|| ||
Db        104 CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVE 160

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              || |:|:|||||:|||:| || | ::|||||||||:||:|:: | |||||||||| ||:|
Db        161 VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP 220

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
              : |||||:|| :::: |::|||||::  |:| || |||: |||| ||| | |:::::||
Db        221 KAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGS 280

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :|:|||| | || |: || |:|||:|| ||||:|:|||| ||||
Db        281 YFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 324


RESULT 12
GC1M_MOUSE
ID   GC1M_MOUSE     STANDARD;      PRT;   393 AA.
AC   P01869;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-1 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80045036; PubMed=115593;
RA   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA   Takahashi N., Mano Y.;
RT   "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT   gamma 1 chain gene.";
RL   Cell 18:559-568(1979).
RN   [2]
RP   SEQUENCE OF 323-393 FROM N.A.
RX   MEDLINE=82197626; PubMed=6804950;
RA   Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT   "mRNA for surface immunoglobulin gamma chains encodes a highly
RT   conserved transmembrane sequence and a 28-residue intracellular
RT   domain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN   [3]
RP   SEQUENCE OF 323-366 FROM N.A.
RX   MEDLINE=82115295; PubMed=6799207;
RA   Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA   Eisenberg D., Wall R.;
RT   "Gene segments encoding transmembrane carboxyl termini of
RT   immunoglobulin gamma chains.";
RL   Cell 26:19-27(1981).
RN   [4]
```

```
RP   SEQUENCE OF 1-44 FROM N.A.
RX   MEDLINE=82222190; PubMed=6283537;
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Membrane-bound;
CC         IsoId=P01869-1; Sequence=Displayed;
CC       Name=Secreted;
CC         IsoId=P01868-1; Sequence=External;
CC         Note=May be the major isoform;
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; V00793; CAA24172.1; -.
DR   EMBL; V00793; CAA24173.1; -.
DR   EMBL; V00793; CAA24174.1; -.
DR   PIR; B02159; G1MSM.
DR   PDB; 15C8; 23-MAR-99.
DR   PDB; 1AE6; 18-MAR-98.
DR   PDB; 1CL7; 12-JAN-00.
DR   PDB; 1F11; 06-FEB-01.
DR   PDB; 1F58; 29-DEC-99.
DR   PDB; 1KC5; 24-JUL-02.
DR   PDB; 1KCR; 11-MAY-02.
DR   PDB; 25C8; 09-JUL-99.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Alternative splicing; Transmembrane; 3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    110       HINGE.
FT   DOMAIN      111    217       CH2.
FT   DOMAIN      218    324       CH3.
FT   DISULFID     27     82
FT   DISULFID    102    102       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID    104    104       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    138    198
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .).
FT   DISULFID    244    302
```

```
FT   TRANSMEM     340     357        POTENTIAL.
FT   DOMAIN       358     393        CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   393 AA;  43386 MW;  4CC88343B7A1CE27 CRC64;

  Query Match             65.6%;  Score 812.5;  DB 1;  Length 393;
  Best Local Similarity   62.3%;  Pred. No. 4.9e-59;
  Matches  139;  Conservative   44;  Mismatches   35;  Indels    5;  Gaps    2;

Qy          7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              | |  |  ||:    |||:||||||| | |: ||:||||||:| :||||:|:|:|| ||
Db        104 CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVE 160

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              || |:|:|||||:|||:| || | ::|||||||||:||:|:: | |||||||||| ||:|
Db        161 VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP 220

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
              : |||||:|| :::: |::|||||::  |:| || |||: ||||  ||| | |:::::||
Db        221 KAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGS 280

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227
              :|:|||| | || |: || |:|||:|| ||||:|:|||| |||
Db        281 YFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG 323


RESULT 13
GCC_RAT
ID   GCC_RAT        STANDARD;      PRT;   329 AA.
AC   P20762;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2C chain C region.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88166903; PubMed=3127222;
RA   Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT   "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT   region cDNA: extensive homology to mouse gamma 3.";
RL   Eur. J. Immunol. 18:317-319(1988).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07189; CAA30169.1; -.
DR   PIR; S00847; S00847.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
```

```
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    113       HINGE.
FT   DOMAIN      114    222       CH2.
FT   DOMAIN      223    329       CH3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    111    111       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    113    113       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    143    203
FT   DISULFID    249    307
SQ   SEQUENCE   329 AA;  36571 MW;  5FCD7B7933850773 CRC64;

  Query Match             65.4%;  Score 809.5;  DB 1;  Length 329;
  Best Local Similarity   63.8%;  Pred. No. 6.9e-59;
  Matches  143;  Conservative   41;  Mismatches   37;  Indels    3;  Gaps    1;

Qy          8 PP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              ||   |   : || ||||:||||||| |||: ||:|||||||||| |:|:|:|:|:|| |
Db        106 PPTDICSCDDNLGRPSVFIFPPKPKDILMITLTPKVTCVVVDVSEEEPDVQFSWFVDNVR 165

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              |  |:|:| ||| | |:|||| | : ||||::|||:||||:|| ||:|||||||| :|:
Db        166 VFTAQTQPHEEQLNGTFRVVSTLHIQHQDWMSGKEFKCKVNNKDLPSPIEKTISKPRGKA 225

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
              | |||||:|| |::::||:|||||:|  |||: |:|||| ||: | :|| | |||||| |
Db        226 RTPQVYTIPPPREQMSKNKVSLTCMVTSFYPASISVEWERNGELEQDYKNTLPVLDSDES 285

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :||||||:||   | :|::::|||:|||||||:|||:|| ||||
Db        286 YFLYSKLSVDTDSWMRGDIYTCSVVHEALHNHHTQKNLSRSPGK 329


RESULT 14
GCAA_MOUSE
ID   GCAA_MOUSE     STANDARD;      PRT;   330 AA.
AC   P01863;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-2A chain C region, A allele.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81076554; PubMed=6777755;
RA   Sikorav J.-L., Auffray C., Rougeon F.;
```

```
RT   "Structure of the constant and 3' untranslated regions of the murine
RT   Balb/c gamma 2a heavy chain messenger RNA.";
RL   Nucleic Acids Res. 8:3143-3155(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81198976; PubMed=6262729;
RA   Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT   "The complete nucleotide sequence of mouse immunoglobin gamma 2a gene
RT   and evolution of heavy chain genes: further evidence for intervening
RT   sequence-mediated domain transfer.";
RL   Nucleic Acids Res. 9:1365-1381(1981).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81223894; PubMed=6787604;
RA   Ollo R., Auffray C., Morchamps C., Rougeon F.;
RT   "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT   suggests that exons can be exchanged between genes in a multigenic
RT   family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN   [4]
RP   MYELOMA PROTEIN MOPC 173.
RX   MEDLINE=74175517; PubMed=4831970;
RA   Bourgois A., Fougereau M., Rocca-Serra J.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin:amino-acid sequence of the Fc fragment. Implications
RT   for the evolution of immunoglobulin structure and function.";
RL   Eur. J. Biochem. 43:423-435(1974).
RN   [5]
RP   DISULFIDE BONDS.
RX   MEDLINE=73056887; PubMed=4565406;
RA   de Preval C., Fougereau M.;
RT   "Determination of the primary structure of a mouse gamma G2a
RT   immunoglobulin. Identification of the disulfide bridges.";
RL   Eur. J. Biochem. 30:452-462(1972).
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00798; CAA24178.1; -.
DR   PIR; A02152; G2MSA.
DR   PDB; 1E4W; 12-JUL-01.
DR   PDB; 1E4X; 12-JUL-01.
DR   PDB; 1MNU; 06-MAY-99.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
```

```
FT   NON_TER       1      1
FT   DOMAIN        6     98       IG-LIKE 1.
FT   DOMAIN      121    220       IG-LIKE 2.
FT   DOMAIN      229    325       IG-LIKE 3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    110    110       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   MOD_RES     330    330       REMOVED POST-TRANSLATIONALLY.
SQ   SEQUENCE   330 AA;  36389 MW;  B84361C5445A6864 CRC64;

  Query Match             65.3%;  Score 809;  DB 1;  Length 330;
  Best Local Similarity   65.2%;  Pred. No. 7.6e-59;
  Matches  146;  Conservative   30;  Mismatches   46;  Indels    2;  Gaps    1;

Qy          7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              |||  |||| ||||||||:|||| || |||| :| ||||||||| :||:|: :|:|: ||
Db        107 CPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVE 166

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              || |:|:   | |||| |||| | : ||||::|||:||||:|| ||||||:|||| ||
Db        167 VHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSV 226

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
              | |||| |||  :|:|| ||:|||:|  | | || ||| :||: | ||| | ||||||||
Db        227 RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS 286

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :|:|||| |:|  | : | :||||:|| ||||:| || | :|||
Db        287 YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330


RESULT 15
GCAM_MOUSE
ID   GCAM_MOUSE     STANDARD;      PRT;   399 AA.
AC   P01865;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-2A chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222190; PubMed=6283537;
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Membrane-bound;
```

```
CC         IsoId=P01865-1; Sequence=Displayed;
CC       Name=Secreted;
CC         IsoId=P01864-1; Sequence=External;
CC         Note=Probably the major isoform;
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00471; AAB59661.1; ALT_INIT.
DR   PIR; A02154; G2MSAM.
DR   PDB; 1KB5; 08-APR-98.
DR   PDB; 1YEE; 15-OCT-97.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing; 3D-structure; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     98       IG-LIKE 1.
FT   DOMAIN      121    220       IG-LIKE 2.
FT   DOMAIN      229    325       IG-LIKE 3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    110    110       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   TRANSMEM    346    363       POTENTIAL.
FT   DOMAIN      364    399       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   399 AA;  44020 MW;  4C38138BFAED3FF0 CRC64;

  Query Match             64.9%;  Score 804;  DB 1;  Length 399;
  Best Local Similarity   65.0%;  Pred. No. 2.5e-58;
  Matches  145;  Conservative   30;  Mismatches   46;  Indels    2;  Gaps    1;

Qy          7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              |||  |||| ||||||||:|||| || |||| :| ||||||||| :||:|: :|:|: ||
Db        107 CPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVE 166

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              || |:|:   | |||| |||| | : ||||::|||:||||:|| ||||||:|||| ||
Db        167 VHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSV 226

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
```

```
                | |||| |||  :|:|| ||:|||:|  | | || ||| :||: | ||| | ||||||||
Db        227 RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS 286

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227
              :|:|||| |:|  | : | :||||:|| ||||:| || | :||
Db        287 YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 329

Search completed: January 16, 2004, 15:57:37
Job time : 19 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 16, 2004, 15:54:50 ; Search time 35 Seconds
(without alignments)
1681.028 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	1233	99.6	471	4	Q8TC77	Q8tc77 homo sapien
2	1233	99.6	701	4	Q96PQ8	Q96pq8 homo sapien
3	1142	92.2	521	4	Q8N4Y9	Q8n4y9 homo sapien
4	1135	91.7	473	4	Q8TC63	Q8tc63 homo sapien
5	1131	91.4	509	4	Q8NF17	Q8nf17 homo sapien
6	909	73.4	337	6	Q95M34	Q95m34 equus cabal
7	831.5	67.2	469	11	Q8R3V9	Q8r3v9 mus musculu
8	828.5	66.9	463	11	Q99LC4	Q99lc4 mus musculu
9	824.5	66.6	437	11	Q9R1A4	Q9r1a4 mus musculu
10	811	65.5	473	11	Q9D8L4	Q9d8l4 mus musculu
11	805	65.0	468	11	Q99L31	Q99l31 mus musculu
12	805	65.0	473	11	Q99L25	Q99l25 mus musculu
13	780	63.0	473	11	Q91Z05	Q91z05 mus musculu
14	780	63.0	474	11	Q8R3H6	Q8r3h6 mus musculu
15	358	28.9	375	4	Q9BSZ1	Q9bsz1 homo sapien
16	358	28.9	597	4	Q9BU10	Q9bu10 homo sapien
17	358	28.9	597	4	Q9BQB8	Q9bqb8 homo sapien
18	358	28.9	597	4	Q96BB9	Q96bb9 homo sapien
19	348	28.1	588	4	Q8WUX4	Q8wux4 homo sapien
20	348	28.1	613	4	Q96EY0	Q96ey0 homo sapien
21	348	28.1	613	4	Q8WUK1	Q8wuk1 homo sapien
22	348	28.1	614	4	Q96GA6	Q96ga6 homo sapien
23	348	28.1	618	4	Q96AA6	Q96aa6 homo sapien
24	347	28.0	613	11	Q8VCX7	Q8vcx7 mus musculu
25	272.5	22.0	684	13	Q90544	Q90544 ginglymosto
26	272	22.0	384	4	Q9UP60	Q9up60 homo sapien
27	272	22.0	493	4	Q8NCL6	Q8ncl6 homo sapien
28	272	22.0	494	4	Q96K68	Q96k68 homo sapien
29	272	22.0	496	4	Q96KX8	Q96kx8 homo sapien
30	269	21.7	496	4	Q96DK0	Q96dk0 homo sapien
31	269	21.7	499	4	Q8N5K4	Q8n5k4 homo sapien
32	267	21.6	416	4	Q9NPP6	Q9npp6 homo sapien
33	267	21.6	497	4	Q8WY24	Q8wy24 homo sapien
34	267	21.6	500	4	Q9BRV0	Q9brv0 homo sapien
35	261	21.1	486	11	Q91Z07	Q91z07 mus musculu
36	261	21.1	487	11	Q99KA4	Q99ka4 mus musculu
37	260	21.0	426	11	Q9DCD9	Q9dcd9 mus musculu
38	253.5	20.5	481	11	Q91WT3	Q91wt3 mus musculu
39	253.5	20.5	481	11	Q91WT1	Q91wt1 mus musculu
40	253.5	20.5	482	11	Q91X92	Q91x92 mus musculu
41	253.5	20.5	482	11	Q8K172	Q8k172 mus musculu
42	253.5	20.5	484	11	Q8VEA0	Q8vea0 mus musculu
43	253.5	20.5	488	11	Q91WR1	Q91wr1 mus musculu
44	253.5	20.5	488	11	Q8K0F2	Q8k0f2 mus musculu
45	253.5	20.5	489	11	Q8VCX4	Q8vcx4 mus musculu

ALIGNMENTS

```
RESULT 1
Q8TC77
ID   Q8TC77       PRELIMINARY;      PRT;   471 AA.
AC   Q8TC77;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
```

```
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024289; AAH24289.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   471 AA;  51791 MW;  388F7F4CF588660E CRC64;

  Query Match             99.6%;  Score 1233;  DB 4;  Length 471;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-108;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 304

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 364

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 424

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        425 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471


RESULT 2
Q96PQ8
ID   Q96PQ8      PRELIMINARY;      PRT;   701 AA.
AC   Q96PQ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Factor VII active site mutant immunoconjugate.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21477448; PubMed=11593034;
```

```
RA   Hu Z., Garen A.;
RT   "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT   cells for immunotherapy in mouse models of prostatic cancer.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR   EMBL; AF272774; AAK58686.1; -.
DR   HSSP; P00761; 1AN1.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR001438; EGF_II.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002383; GLA_blood.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   InterPro; IPR000294; VitK_dep_GLA.
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00594; gla; 1.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00010; EGFBLOOD.
DR   PRINTS; PR00001; GLABLOOD.
DR   SMART; SM00179; EGF_CA; 1.
DR   SMART; SM00069; GLA; 1.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00010; ASX_HYDROXYL; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01187; EGF_CA; 1.
DR   PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   EGF-like domain; Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   701 AA;  77826 MW;  94AC6CEB42CC992F CRC64;

  Query Match             99.6%;  Score 1233;  DB 4;  Length 701;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-108;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 534

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 594

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        595 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 654

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 701


RESULT 3
Q8N4Y9
ID   Q8N4Y9      PRELIMINARY;      PRT;   521 AA.
AC   Q8N4Y9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells from Tonsils;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC033178; AAH33178.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   521 AA;  57156 MW;  2AC7D22E72D6CAA2 CRC64;

  Query Match            92.2%;  Score 1142;  DB 4;  Length 521;
  Best Local Similarity  92.1%;  Pred. No. 1.8e-99;
  Matches  209;  Conservative    9;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |    || |||||||||||||||||||||||||||||||||||||||||||:| ||||
Db        295 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 354

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||:|||:||||||||||||||||||||||||||||||||||| |
Db        355 GVEVHNAKTKPREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 414

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||:|:|||||||||||||||||||||:||||||| ||||:|||
Db        415 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 474

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||:|||||||||||| :||||||||||
Db        475 DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK 521
```

```
RESULT 4
Q8TC63
ID   Q8TC63      PRELIMINARY;      PRT;   473 AA.
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00196; COPPER_BLUE; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51986 MW;  E29920B09BA369F5 CRC64;

  Query Match           91.7%;  Score 1135;  DB 4;  Length 473;
  Best Local Similarity  93.7%;  Pred. No. 7.1e-99;
  Matches  208;  Conservative    8;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
              || ||||| |||||||||||||||||||||||||||||||| |||||:||||||||||||
Db        252 CPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH 311

Qy         67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
              ||||||||||:|||||||||||||||||||||||||||| ||: ||||||||||||||
Db        312 NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE 371

Qy        127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 186
              |||||||||::|:||||||||||||||||||||||||||||||||||||||||||||||
Db        372 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 431

Qy        187 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||:|||||||||:|||||||||||||||||||||||||| ||
Db        432 LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 473


RESULT 5
Q8NF17
ID   Q8NF17      PRELIMINARY;      PRT;   509 AA.
AC   Q8NF17;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
```

```
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   FLJ00385 protein (Fragment).
GN   FLJ00385.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT   "The nucleotide sequence of a long cDNA clone isolated from human
RT   spleen.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK090464; BAC03445.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   509 AA;  56111 MW;  089498D8076E863C CRC64;

  Query Match             91.4%;  Score 1131;  DB 4;  Length 509;
  Best Local Similarity   92.0%;  Pred. No. 1.9e-98;
  Matches  207;  Conservative    9;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |    || |||||||||||||||||||||||||||||||||||||||||||:| ||||
Db        214 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 273

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||:|||:||||||||||||||||||||||||||||||||||||| |
Db        274 GVEVHNAKTKPREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 333

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||:|:||||||||||||||||||||||:||||||| ||||:|||
Db        334 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 393

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 226
              ||||||||||||||||||||:|||||||||||| :|||||||||
Db        394 DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSP 438


RESULT 6
Q95M34
ID   Q95M34      PRELIMINARY;      PRT;   337 AA.
AC   Q95M34;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Immunogobulin gamma 1 heavy chain constant region (Fragment).
GN   IGHC1.
OS   Equus caballus (Horse).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wagner B.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98383416; PubMed=9717671;
RA   Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA   Leibold W., Radbruch A.;
RT   "Organization of the equine immunoglobulin heavy chain constant region
RT   genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL   Immunobiology 199:105-119(1998).
DR   EMBL; AJ300675; CAC44624.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
FT   NON_TER       1       1
SQ   SEQUENCE   337 AA;  37438 MW;  A60BF2B01DEFD1F6 CRC64;

  Query Match             73.4%;  Score 909;  DB 6;  Length 337;
  Best Local Similarity   71.9%;  Pred. No. 1.1e-77;
  Matches  161;  Conservative   32;  Mismatches   29;  Indels    2;  Gaps    1;

Qy          7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
              || |||||||||||||:||| |||||||:||||||||||||| |:|:|||||||:|||||
Db        114 CPKCPAPELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSQENPDVKFNWYMDGVEVR 173

Qy         67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
               | |:|:|||:|||||||||| : |||||:|||:||||:|:||| |||:||:| ||: :|
Db        174 TATTRPKEEQFNSTYRVVSVLRIQHQDWLSGKEFKCKVNNQALPQPIERTITKTKGRSQE 233

Qy        127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGS 184
              |||| | |  |||:|::||:||||| ||| :| :||:|||||  |  | ||    |||||
Db        234 PQVYVLAPHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGS 293

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :||||||:||::|||||  |:| ||||||||||||::| :|||
Db        294 YFLYSKLSVDRNRWQQGTTFTCGVMHEALHNHYTQKNVSKNPGK 337


RESULT 7
Q8R3V9
ID   Q8R3V9      PRELIMINARY;      PRT;   469 AA.
AC   Q8R3V9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical 52.0 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024405; AAH24405.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   469 AA;  51976 MW;  534793F155D05457 CRC64;

  Query Match             67.2%;  Score 831.5;  DB 11;  Length 469;
  Best Local Similarity   63.8%;  Pred. No. 3.5e-70;
  Matches  143;  Conservative   41;  Mismatches   35;  Indels    5;  Gaps    2;

Qy          7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              | |  |  ||:    |||:||||||| | |: ||:||||||:| :||||:|:|:|| ||
Db        249 CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVE 305

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              || |:|||||||:|||:| || | ::|||||||||:||:|:: | |||||||||| ||:|
Db        306 VHTAQTKPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP 365

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
              : |||||:|| :::: |::|||||::  |:| || |||: ||||  ||| | |::|:|||
Db        366 KAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGS 425

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :|:|||| | || |: || |:|||:|| ||||:|:|||| ||||
Db        426 YFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 469


RESULT 8
Q99LC4
ID   Q99LC4      PRELIMINARY;      PRT;   463 AA.
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003435; AAH03435.1; -.
DR   HSSP; P01842; 7FAB.
```

```
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   463 AA;  51007 MW;  EAA674C6BBC30783 CRC64;

  Query Match             66.9%;  Score 828.5;  DB 11;  Length 463;
  Best Local Similarity   63.4%;  Pred. No. 6.6e-70;
  Matches  142;  Conservative   42;  Mismatches   35;  Indels    5;  Gaps    2;

Qy          7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              | |  |  ||:    |||:||||||| | |: ||:|||||||:| :||||:|:|:|| ||
Db        243 CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVE 299

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              || |:|:|||||:|||:| || | ::|||||||||:||:|:: | |||||||||| ||:|
Db        300 VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP 359

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
              : |||||:|| :::: |::|||||::  |:| || |||: ||||  ||| | |::|:|||
Db        360 KAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGS 419

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :|:|||| | || |: || |:|||:|| ||||:|:|||| ||||
Db        420 YFIYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 463


RESULT 9
Q9R1A4
ID   Q9R1A4      PRELIMINARY;      PRT;   437 AA.
AC   Q9R1A4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Gamma1 heavy chain of Mab7 (Fragment).
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFV).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152372; AAD40243.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
```

```
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
FT   NON_TER       1      1
FT   NON_TER     437    437
SQ   SEQUENCE   437 AA;  48142 MW;  5C3A7BB3EE7D697C CRC64;

  Query Match             66.6%;  Score 824.5;  DB 11;  Length 437;
  Best Local Similarity   62.9%;  Pred. No. 1.5e-69;
  Matches  141;  Conservative   43;  Mismatches   35;  Indels    5;  Gaps    2;

Qy          7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              | |  |  ||:    |||:||||||| | |: ||:||||||:| :||||:|:|:|| ||
Db        217 CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVE 273

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              || |:|:|||||:|||:| || | ::|||||||||:||:|:: | |||||||||| ||:|
Db        274 VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP 333

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
              : |||||:|| :::: |::|||||::  |:| || |||: ||||  ||| | |::|:|||
Db        334 KAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGS 393

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :|:|||| | || |: || |:|||:|| ||||:|:|:|| ||||
Db        394 YFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKNLSHSPGK 437


RESULT 10
Q9D8L4
ID   Q9D8L4      PRELIMINARY;      PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   1810060O09Rik protein.
GN   IGH-1 OR 1810060O09RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
```

```
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007918; BAB25349.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   473 AA;  51699 MW;  9DED57A514475FBB CRC64;

  Query Match             65.5%;  Score 811;  DB 11;  Length 473;
  Best Local Similarity   64.0%;  Pred. No. 3.1e-68;
  Matches  142;  Conservative   38;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
              |||| ||:||||||||:|||| || |||| :| |||||||| :||:|: :|:|: ||||
Db        252 CPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVH 311

Qy         67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
               |:|:   | |||| |||| | : ||||::|||:||||:|:|||:|||||||| :|  |
Db        312 TAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRA 371

Qy        127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 186
              |||| |||  :|:|| : ||||:: || |::|||:| |||: | ||| |  |||||||:|
Db        372 PQVYVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSYF 431

Qy        187 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :|||| | || |::|::|:|||:|| |||| | |::| | ||
Db        432 MYSKLRVQKSTWERGSLFACSVVHEGLHNHLTTKTISRSLGK 473


RESULT 11
Q99L31
ID   Q99L31      PRELIMINARY;      PRT;   468 AA.
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
```

```
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   468 AA;  51661 MW;  96352328B3332ADB CRC64;

  Query Match             65.0%;  Score 805;  DB 11;  Length 468;
  Best Local Similarity   65.2%;  Pred. No. 1.1e-67;
  Matches  146;  Conservative   30;  Mismatches   46;  Indels    2;  Gaps    1;

Qy          7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              |||  |||| ||||||||:|||| || |||| :| ||||||||| :||:|: :|:|: ||
Db        245 CPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVE 304

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              |  |:|:   | |||| |||| | : ||||::|||:||||:||||||||:|||| ||
Db        305 VLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPKGSV 364

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
              | |||| |||  :|:|| ||:|||:|  | | || ||| :||: | ||| | ||||||||
Db        365 RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS 424

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :|:|||| |:|  | : | :||||:|| ||||:| || | :|||
Db        425 YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 468


RESULT 12
Q99L25
ID   Q99L25      PRELIMINARY;      PRT;   473 AA.
AC   Q99L25;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003888; AAH03888.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
```

```
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   473 AA;  52449 MW;  BE9889B7986DA155 CRC64;

  Query Match             65.0%;  Score 805;  DB 11;  Length 473;
  Best Local Similarity   65.2%;  Pred. No. 1.1e-67;
  Matches  146;  Conservative   30;  Mismatches   46;  Indels    2;  Gaps    1;

Qy          7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
              |||  |||| ||||||||:|||| || |||| :| ||||||||| :||:|: :|:|: ||
Db        250 CPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVE 309

Qy         65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
              |  |:|:   | |||| |||| | : ||||::|||:||||:||||||||:|||| ||
Db        310 VLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPKGSV 369

Qy        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
              | |||| |||  :|:|| ||:|||:|  | | || ||| :||: | ||| | ||||||||
Db        370 RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS 429

Qy        185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              :|:|||| |:|  | : | :||||:|| ||||:| || | :|||
Db        430 YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 473


RESULT 13
Q91Z05
ID   Q91Z05      PRELIMINARY;      PRT;   473 AA.
AC   Q91Z05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical 51.9 kDa protein.
GN   AU044919.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010327; AAH10327.1; -.
DR   MGD; MGI:2144967; AU044919.
DR   InterPro; IPR000345; CytC_heme_bind.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51946 MW;  CF625F008932AF12 CRC64;

  Query Match             63.0%;  Score 780;  DB 11;  Length 473;
  Best Local Similarity   61.8%;  Pred. No. 2.6e-65;
```

```
  Matches  141;  Conservative   34;  Mismatches   47;  Indels    6;  Gaps    1;

Qy          7 CPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              |||      |||| | ||||||:|||  || |||| ||:|||||||| :||:|: :|:|
Db        246 CPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFV 305

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              : |||| |:|:   | |||| |||| | : ||||::|||:||||:|| ||:|||:||||
Db        306 NNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKI 365

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||  | |||| |||  ::|::  ||||||| || | ||:||| |||  | ||| | ||||
Db        366 KGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLD 425

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||:|:|||| :  |:|:: : |||:| || | |:| :|::| ||||
Db        426 SDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 473


RESULT 14
Q8R3H6
ID   Q8R3H6      PRELIMINARY;      PRT;   474 AA.
AC   Q8R3H6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical 51.7 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025447; AAH25447.1; -.
DR   InterPro; IPR000345; CytC_heme_bind.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   474 AA;  51748 MW;  8608B57C6CD2874A CRC64;

  Query Match           63.0%;  Score 780;  DB 11;  Length 474;
  Best Local Similarity  61.8%;  Pred. No. 2.6e-65;
  Matches  141;  Conservative   34;  Mismatches   47;  Indels    6;  Gaps    1;

Qy          7 CPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              |||      |||| | ||||||:|||  || |||| ||:|||||||| :||:|: :|:|
Db        247 CPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFV 306

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
```

```
                : |||| |:|:   | |||| |||| | : ||||::|||:||||:|| ||:|||:||||
Db        307 NNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKI 366

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||  | |||| |||  ::|::  ||||||| || | ||:||| |||  | ||| | ||||
Db        367 KGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLD 426

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||:|:|||| :  |:|:: : |||:| || | |:| :|::| ||||
Db        427 SDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 474


RESULT 15
Q9BSZ1
ID   Q9BSZ1      PRELIMINARY;      PRT;   375 AA.
AC   Q9BSZ1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC004476; AAH04476.1; -.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   375 AA;  41314 MW;  B1A0A0998F473619 CRC64;

  Query Match           28.9%;  Score 358;  DB 4;  Length 375;
  Best Local Similarity  34.1%;  Pred. No. 1.5e-25;
  Matches   73;  Conservative   48;  Mismatches   85;  Indels    8;  Gaps    6;

Qy         21 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 80
              ||  ||    :: :::: ::||:| |::  |  |  :|     |     |   |   |:|
Db        146 VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESHPNAT 203

Qy         81 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPSRDEL 139
              :  |   ::   || :|: : | |::  ||:|:::|||: ||     | || |||:|::|
Db        204 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQL 263

Qy        140 T-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSKLTVD 194
                :   ::|||| || |:|: |:|   |||     | |: |: :  : | :| :| |||
Db        264 NLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVS 323
```

```
Qy         195 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
               :  |  |  ::| | |||| |  |::::  | ||
Db         324 EEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK 357
```

Search completed: January 16, 2004, 15:58:27
Job time : 38 secs